

2 32  
CTT TCA GAA GCC CGG GAG AGC GTC TTG GGG GAT TTG CTG AAG GTT GTG CTG TAC AGC CTG  
leu ser glu ala arg glu ser val leu gly asp leu leu lys val val leu tyr ser leu

62 92  
GGC AGT GCC CAG AGT GCC CTC TTC TTG CAG CAT GGC CTG GCC ACC CAG AGG GCC CTT GTG  
gly ser ala gln ser ala leu phe leu gln his gly leu ala thr gln arg ala leu val

122 152  
TCC AAG TTC CCG GAG CTG CTG TTC GAG GAG GAC ACG GAG CTG TGT GCC GAC CTG TGC CTG  
ser lys phe pro glu leu leu phe glu glu asp thr glu leu cys ala asp leu cys leu

182 212  
AGG CTC CTA CGA CAC TGT GGC AGC CGC ATC AGC ACC ATC CGC ACG CAC GCC AGC GCC TCG  
arg leu leu arg his cys gly ser arg ile ser thr ile arg thr his ala ser ala ser

242 272  
CTG TAC CTG CTC ATG CGA CAG AAC TTC GAG ATC GGC CAC AAC TTT GCC CGT GTG AAG ATG  
leu tyr leu leu met arg gln asn phe glu ile gly his asn phe ala arg val lys met

302 332  
CAG GTC ACC ATG TCT CTC TCG TCC CTG GTG GGG ACG ACG CAG AAC TTC AGT GAA GAG CAC  
gln val thr met ser leu ser ser leu val gly thr thr gln asn phe ser glu glu his

362 392  
CTG CGA CGT TCA CTC AAA ACC ATC CTC ACC TAT GCT GAG GAG GAC ATG GGG CTG CGG GAC  
leu arg arg ser leu lys thr ile leu thr tyr ala glu glu asp met gly leu arg asp

422 452  
AGC ACC TTC GCA GAG CAG GTC CAG GAC CTG ATG TTC AAC CTG CAC ATG ATC CTG ACG GAC  
ser thr phe ala glu gln val gln asp leu met phe asn leu his met ile leu thr asp

482 512  
ACG GTG AAG ATG AAG GAA CAC CAG GAG GAC CCT GAG ATG CTC ATC GAC CTC ATG TAC AGA  
thr val lys met lys glu his gln glu asp pro glu met leu ile asp leu met tyr arg

542 572  
ATT GCC CGG GGC TAC CAG GGC TCA CCG GAC CTT CGG CTG ACC TGG TTG CAG AAC ATG GCC  
il ala arg gly tyr gln gly ser pro asp leu arg leu thr trp leu gln asn met ala

602 |xxxxxxxxxxxxxxxxx transmembrane domain xxxxxxxxxxxxxx  
GGG AAG CAC GCG GAG CTG GGC AAC CAC GCC GAG GCC GCC CAG TGC ATG GTG CAC GCG GCC  
gly lys his ala glu leu gly asn his ala glu ala ala gln cys met val his ala ala

XXXXXXXXXXXXXXXXXXXXXXXXXXXXX|

692

GCC CTC GTG GCT GAG TAC CTC GCC CTG CTC GAG GAC CAC CGC CAC CTG CCC GTG GGC TGC  
ala leu val ala glu tyr leu ala leu l u glu asp his arg his leu pro val gly cys

722

752

GTT TCC TTC CAG AAC ATC TCA TCC AAT GTG CTA GAG GAG TCC GCC ATC TCC GAC GAC ATC  
val ser phe gln asn ile ser ser asn val leu glu glu ser ala ile ser asp asp ile

782

812

CTG TCG CCC GAC GAG GAG GGC TTC TGC TCC GGG AAG CAC TTC ACT GAG CTG GGG CTG GTA  
leu ser pro asp glu glu gly phe cys ser gly lys his phe thr glu leu gly leu val

842

872

GGG TTG CTG GAA CAG GCA GCC GGC TAC TTC ACC ATG GGC GGG CTC TAC GAG GCG GTG AAT  
gly leu leu glu gln ala ala gly tyr phe thr met gly gly leu tyr glu ala val asn

902

932

GAG GTC TAC AAG AAC CTC ATC CCC ATC CTG GAA GCC CAC CGT GAC TAC AAG AAG CTG GCC  
glu val tyr lys asn leu ile pro ile leu glu ala his arg asp tyr lys lys leu ala

962

992

CCG GTG CAC GGC AAA CTG CAG GAG GCC TTC ACC AAG ATC ATG CAC CAG AGT TCC GGC TGG  
ala val his gly lys leu gln glu ala phe thr lys ile met his gln ser ser gly trp

1022

|xxxxx ITAM xxxxx|1052

GAG CGC GTG TTC GGG ACG TAT TTC CGC GTG GGC TTC TAC GGC GCC CAC TTC GGT GAC CTG  
glu arg val phe gly thr tyr phe arg val gly phe tyr gly ala his phe gly asp leu

1082

1112

GAT GAG CAG GAG TTT GTG TAC AAG GAG CCA TCG ATC ACG AAG CTG GCA GAG ATC TCA CAC  
asp glu gln glu phe val tyr lys glu pro ser ile thr lys leu ala glu ile ser his

1142

1172

CGG CTG GAG GAG TTC TAC ACG GAG AGA TTT GGC GAC GAC GTC GTT GAG ATT ATC AAA GAC  
arg leu glu glu phe tyr thr glu arg phe gly asp asp val val glu ile ile lys asp

1202

1232

TCT TAC CCT GTG GAC AAG TCC AAG CTT GAC TCA CAA AAG GCC TAC ATC CAG ATC ACG TAT  
ser tyr pro val asp lys ser lys leu asp ser gln lys ala tyr ile gln ile thr tyr

1262

1292

GTG GAA CCG TAC TTT GAT ACC TAC GAG CTC AAG GAC CGG GTG ACC TAC TTT GAC CGC AAC  
val glu pro tyr phe asp thr tyr glu leu lys asp arg val thr tyr phe asp arg asn

1322

1352

TAT GGG CTT CGC ACA TTC CTG TTC TGC ACG CCG TTC ACG CCG GAT GGG CGC GCA CAC GGG  
tyr gly leu arg thr phe leu phe cys thr pro phe thr pro asp gly arg ala his gly

1382 1412  
GAG CTG CCC GAG CAA CAC AAG CGT AAG ACG CTG CTC AGC ACC GAC CAC GCC TTC CCC TAC  
glu 1 u pro glu gln his lys arg lys thr leu leu ser thr asp his ala ph pro tyr

1442 1472 |xxxxxxxxxxx  
ATC AAG ACT CGC ATC CGT GTG TGC CAC CGG GAG GAG ACG GTG CTG ACG CCA GTG GAG GTG  
ile lys thr arg ile arg val cys his arg glu glu thr val leu thr pro val glu val

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coile coil 1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx  
GCC ATC GAG GAC ATG CAG AAG AAG ACA CGG GAG CTG GCC TTT GCC ACC GAG CAG GAC CCA  
ala ile glu asp met gln lys lys thr arg glu leu ala phe ala thr glu gln asp pro

xx|  
CCA GAT GCT AAG ATG CTA CAG ATG GTG CTT CAG GGC TCT GTA GGG CCC ACC GTG AAC CAG  
pro asp ala lys met leu gln met val leu gln gly ser val gly pro thr val asn gln

1622 1652  
GGT CCC CTG GAG GTG GCC CAG GTG TTT TTA GCA GAG ATC CCG GAA GAC CCC AAG CTC TTC  
gly pro leu glu val ala gln val phe leu ala glu ile pro glu asp pro lys leu phe

1682 1712  
CGG CAT CAC AAC AAA TTG CGG CTC TGC TTC AAG GAC TTC TGC AAG AAA TGT GAG GAT GCG  
arg his his asn lys leu arg leu cys phe lys asp phe cys lys lys cys glu asp ala

xx Coiled coil 2 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx  
CTG CGG AAA AAT AAG GCC CTG ATT GGG CCG GAC CAG AAG GAG TAC CAC CGT GAG CTG GAG  
leu arg lys asn lys ala leu ile gly pro asp gln lys glu tyr his arg glu leu glu

xx|  
CGC AAC TAC TGC CGC CTG CGG GAG GCT CTG CAG CCC CTG CTT ACC CAG CGC CTG CCC CAG  
arg asn tyr cys arg leu arg glu ala leu gln pro leu leu thr gln arg leu pro gln

1862 1892  
CTG ATG GCA CCC ACC CCA CCC GGC CTC AGG AAC TCC TTG AAC AGA GCA AGT TTC CGA AAG  
leu met ala pro thr pro pro gly leu arg asn ser leu asn arg ala ser phe arg lys

1922 1952  
GCA GAC CTC TGA GCC CAC AAG GAC CAA AGC TGT ACC TAG AGG AAC CAG CAC CCG GGC CTC  
ala asp leu STP

1982 2012  
AGC TGT CTG TGC TGC GAG GGG AGT CTG CCC TGG TGC CCA CTG GGC TGT GGG GTG ACC ACA

2042 2072  
CTG TAC TTG GGG CTG GGC CCT CTG CCC CTG TGT CCC CAT CTG TGT GCA CTG ATG CTT CCT

2102 2132  
CCC TTT TTT AAT TTA AAA TGG TTT TTA TAA GCA AAA AAA AAA AAA AAA

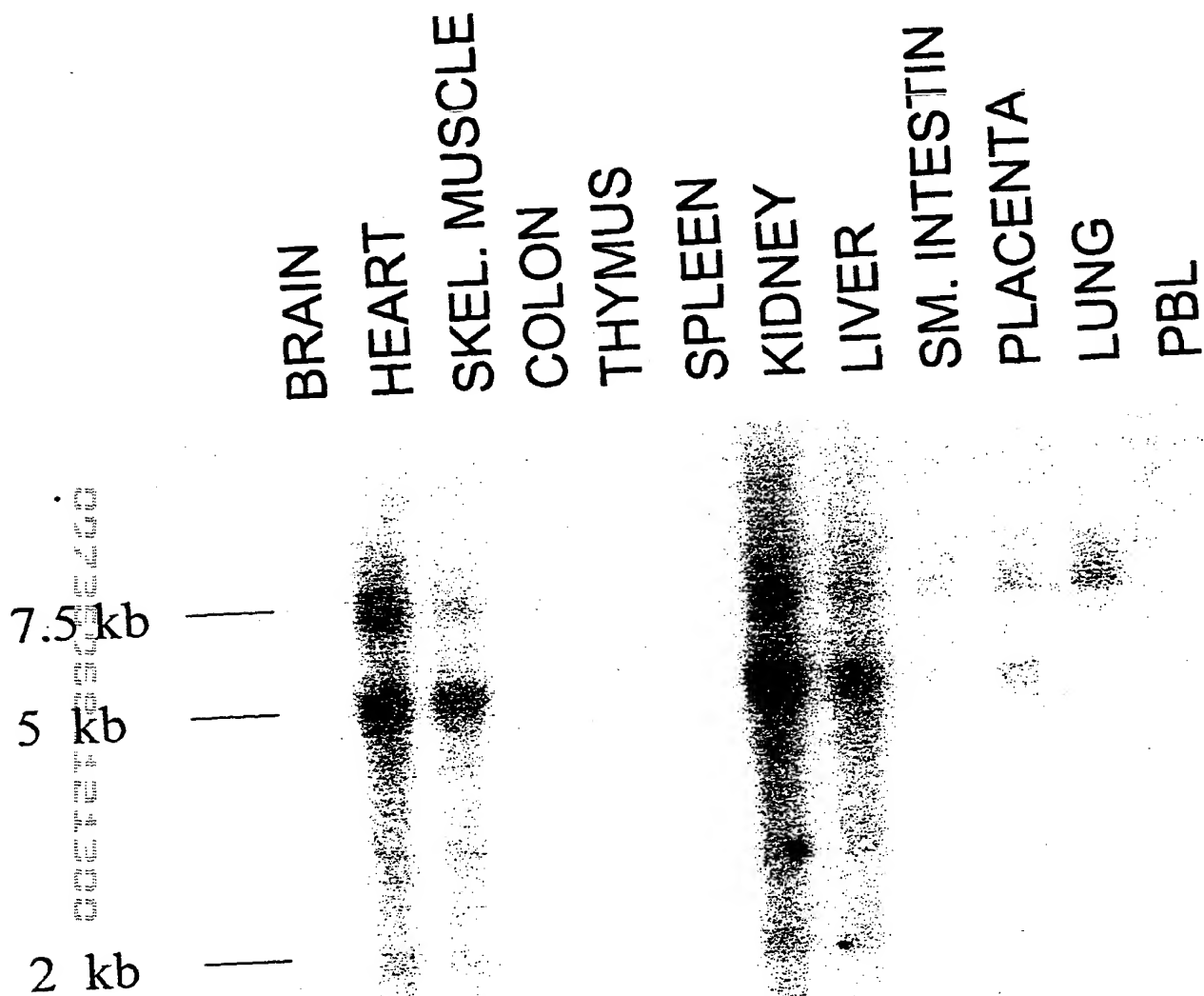


FIG. 2

HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVPKYLKYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----VLHHHQNPEFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVETRSAFAAVLHHHQNPEFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	IELPTQLHEKHHLTFFHVSCDNSSKSGSTKKRDVVETQVGYSWLPLLKDRVVTSEQHI
KIAA	IELPTQLHEKHHLTFFHVSCDNSSKSGSTKKRDVVETQVGYSWLPLLKDRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC
KIAA	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSISLISNSARV
HC5	-----

HC2A	OKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	OKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWNTGGPKAAPWGSNPSPSAES
HC5	-----

HC2A I I H V V A Q C N G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E K S M T T I L K P S A D F L T S N  
 KIAA I I H V V A Q C H E E G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E L T K S M T T I L K P S A D F L T S N  
 rat -----  
 HC4 L F H I V S K C H E E G L D S Y L S S F I K Y S F R P G K P S A P Q A P L I H E T L A T M M I A L L K Q S A D F L A I N  
 HC1 L P D I V A K C H E E Q L D H S V Q S Y I K F V F K T R --- A C K E R P V H E D L A K N V T G L L K - S N D S P T V K  
 HC3 T Q A M D R S C N R M S S H T E T S S F L Q T L T G R L P --- T K K L F H E E L A L Q W V V C S G -- S V R --- E  
 HC5 -----

Cadherin  
 Cleavage

HC2A K L L R Y S W F F F D V L I K S M A Q H L I E N S K V K L I R N Q R F P A S Y H H A A E T V V N M L M P H I T Q K F G D  
 KIAA K L L K Y S W F F F D V L I K S M A Q H L I E N S K V K L I R N Q R F P A S Y H H A V E T V V N M L M P H I T Q K F R D  
 rat -----  
 HC4 K L L K Y S W F F F E I I A K S M A T Y L L E E N K I K L T H G Q R F P K A Y H H A L H S L F L A I T - I V E S Q Y A E  
 HC1 H V L K H S W F F F A I I L K S M A Q H L I D T N K I Q L E R P Q R F P E S Y Q N E L D N L V M V L S D H V I W K Y K D  
 HC3 S A L Q Q A W F F F E L M V K S M V H H L Y F N D K L E A P R K S R F P E R F M D D I A A L V S T I A S D I V S R F Q K  
 HC5 -----

HC2A N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S -- C F A P G D P K T L F E Y K F E F L  
 KIAA N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S -- C F A P G D P K T L F E Y K F E F L  
 rat -----  
 HC4 I P K E S R N V N Y S L A S F L K C C L T L M D R G F V F N L I N --- D Y I S -- G F S P K D P K V L A E Y K F E F L  
 HC1 A L E E T R R A T H S V A R F L K R C F T F M D R G C V F K M V N --- N Y I S -- M F S S G D L K T L C Q Y K F D F L  
 HC3 D T E M V E R L N T S L A F F L N D L L S V M D R G F V F S L I K S C Y Q V S S K L Y S L P N P S V L V S L R L D F L  
 HC5 -----

HC2A R V V C N H E H Y I P L N L P M --- P F G K G R I Q R --- Y Q D L Q L --- D Y S L T D E F  
 KIAA R V V C N H E H Y I P L N L P M --- P F G K G R I Q R --- Y Q D L Q L --- D Y S L T D E F  
 rat -----  
 HC4 Q T I C N H E H Y I P L N L P M --- A F A K P K L Q R --- V Q D S N L --- E Y S L S D E Y  
 HC1 Q E V C Q E H F I P L C L P I R S A N I P D P L T P S E S --- T Q E L H A S D M P E Y S V T N E F  
 HC3 R I I C S H E H Y V T L N L P C S L L T P P A S P S P S V S S A T S Q S S G F S T N V Q D Q K I A N M F E L S -- V P F  
 HC5 ----- M N A D T A P T S P C P S I S --- S Q N S S S C S S F Q D Q K I A S M F D R T S R V P A

Cadherin  
 EC motif

HC2A C R N H F L V G L L L R E V G T A L Q E F R E --- V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T  
 KIAA C R N H F L V G L L L R E V G T A L Q E F R E --- V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T  
 rat -----  
 HC4 C K H H F L V G L L L R E T S I A L Q D N Y E --- I R Y T A I S V I K N L L I K H A F D T R Y Q H K N Q Q A K I A Q  
 HC1 C R K H F L I G I L L R E V G F A L Q E D Q D --- V R H L A V L K N L M A K H S F D D R Y R E P R K Q A Q I A S  
 HC3 R Q Q H Y L A G I V L T E L A V I L D P D A E G L F G L H K K V I N M V H N L L S S H D S D P R Y S D P Q I K A R V A M  
 HC5 S S T S - S P G L F T E L A A A L D A E G E G I S E V Q R K A V S A I H S L L S S H D L D P R C V K P E V K V K I A A

HC2A L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H  
 KIAA L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H  
 rat -----  
 HC4 L Y L P F V G L L L E N I Q R L A G R D T L Y S C A A M P N S A S R D E F P C G --- F T S P -- A N -- R G S L S  
 HC1 L Y M P L Y G M L L D N M P R I Y L K D L Y P F T V N T S N Q G S R D D L S T N G G F Q S Q T A I K H A N S V D T S F S  
 HC3 L Y L P L I G I M E T V P Q L Y D F T E T H N Q R G R P I C I A T D D Y E S E --- S G --- S M I S  
 HC5 L Y L P L V G I I L D A L P Q L C D F T V A D T R R Y R --- T S G S D E E Q E --- G A --- G A I T

HC2A	KDLLGAISG	●	PYTTSTPNINSVRNADSRGSLISTDSGNS	●	ARNSEKSNSLDKHQSS
KIAA	KDLLGAISG	●	PYTTSTPNINSVRNADSRGSLISTDSGNS	●	ARNSEKSNSLDKHQSS
rat	-----				
HC4	TDKDTAYGSFQNG	-----	HGIKREDSRGS	LIP-EGATGFPDQGN	TGEN-----TRQS
HC1	KDVLNSIAAFSS	-----	IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL		
HC3	QTVAMAIAGTSVPQ	-----	LTRPGSFLLTSTSGRQHT		
HC5	QNVALAIAGNNFN	-----	LKTSG-IVLSSLPYKQYN		
HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTI	SEVCL			
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTI	SEVCL			
rat	-----				
HC4	STRSSVSQYNRLDQYEIRSLLMCYLYIVKMI	SEDTLTYWN-KVSPQELINILILLEVCL			
HC1	ALIGSTLRFDRLDQAE	TRSLLMCFHIMKTI SYETLIAYWQ-RAPSPEVSDFFSILDVCL			
HC3	-----T	FSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQLNRLDLLLYLCV			
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV				
HC2A	HQFOYMGKRYIARNQ	EGLG--PIVHDRKS-----		QTLPVSRNRTGMM	
KIAA	HQFOYMGKRYIAR	-----		TGM	
rat	-----				
HC4	FHFRYMGKRNIARVHDAWLSKHFGIDRKS	-----		QTMPALNRNSGVM	
HC1	QNFRLGKRNIIRKIAAF--KFVQSTQ	NNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHK			
HC3	SCFEYKGGKVFERMNSLTFK--KSKDMRAK	-----		LEEAILGSIGARQEMV	
HC5	LCFEYKGGQSSDKVSTQVLQ--KSRDVKAR	-----		LEEALLRGEARGEMM	
HC2A	HARLQQL	-----	GSLDNS-----	LTFNHSYGHSDADVLHQSLLEANIATEVC	
KIAA	HARLQQL	-----	GSLDNS-----	LTFNHSYGHSDADVLHQSLLEANIATEVC	
rat	-----				
HC4	QARLQHL	-----	SSLESS-----	FTLNHSSTTTEADI FHQALLEGNTATEVS	
HC1	QHRSTLPIIRGK--NALS	NPKL----LQMLDNTMTS		NSNEIDIVHHVDTEANIATEGC	
HC3	RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQ	NTEKLDKSRAEIEHEALIDGNLATEAN			
HC5	RRRAPGNDRFP----	GLNENLRWKKEQTHWRQANEKLDKTKAELDQ		EALISGNLATEAH	
HC2A	LTALDTLSLFTLAFKNQLLADHGHNP	LMKKVFDVYLCFLQKHQSETALKNVFTALRS		LIY	
KIAA	LTALDTLSLFTLAFKNQLLADHGHNP	LMKKVFDVYLCFLQKHQSETALKNVFTALRS		LIY	
rat	-----KLSRGHSP				
HC4	LTVLDTISFFTQCFKTHFLNNDGHNP	LMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS			
HC1	LTILDVLSLFTQTHQRLQOCDCQNSLMKRG	FDTYMLFFQVQNQSATALKHVFASLRLFVC			
HC3	LIILDTLEIVVQTVS--VTES--KESILGGVLK	VLLHSMACNQSAVYLQHC		FATORALVS	
HC5	LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNC	DQSTTYLTHCFATL		RALIA	
HC2A	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRN	NFDYTGKKS		FVRTH	
KIAA	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRN	NFDYTGKKS		FVRTH	
rat	KFPSTFYEGRADMCAALCYEVLKCCNSKLSSIRTEASQLLYFLMRN				
HC4	KFPSTFYEGRADMCAALCYEVLKCCNSKLSSIRTEASQLLYFLMRN	NFDYTGKKS		FVRTH	
HC1	KFPSAFFQGPADLCGSFCYEVLKCCNHR	SRSTQTEASALLYLFMRKNFEFNKQKSIVRSH			
HC3	KFPELLFEEETEQCADLCRLRLRHCS	SSIGTIRSHPSASLYLLMRQNF		EIGN--NFARVK	
HC5	KFGDLLFEEVEQCFDLCHQVLHHCSS	SMDVTRSQACATLYLLMRFS		FGATS--NFARVK	
HC2A	LQVIISVSQLIADVVGIGETR	FQQSLSIINN		CANSDRLIKHTSFSSDVKDLTKRIRTVLM	
KIAA	LQVIISVSQLIADVVGIGETR	FQQSLSIINN		CANSDRLIKHTSFSSDVKDLTKRIRTVLM	
rat	LQVIISLSQLIADVVGIGETR				
HC4	LQIIIAVSQLIADVALSGGSRFQESLFIINN	FANS		DRPMLARAPAEVKDLTKRIRTVLM	
HC1	LQLIKAVSQLIAD-AGIGGSRFQHS	LAITNNFANGDKQMKNSN		FPAEVKDLTKRIRTVLM	
HC3	MQVPMSLSSLVGTSQNFNEEFLRRSLK	TILTYAEEDLELRETT		FPDQVQDLVFNLMILS	
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQ	MTPFPTQVEELL		CNLSILY	

FIG. 3  
3 of 5

		Transmembrane
HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGL	LSEAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGL	LSEAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGL	LSEAAMCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLD MAKIHVKNGL	FSEAAMCYVHV
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLES MAKIHARNGD	LSEAAMCYIHI
HC3	DTVKMKEHQEDPEMLIDL MYRIAKGYQTS PDLRLTWLQNMAGKHSERSN	HAEAAQCLVHS
HC5	DTVKMREFQEDPEMLMDL MYRIAKSYQAS PDLRLTWLQNMAEKHTKKKQ	YTEAMCLVHA

	domain	SH3	
HC2A	TALVAEYILTRKGV-----		FRQGCTAFRVITPN
KIAA	TALVAEYILTRKEA-----	-VQWEPPLLP HSHSACLRRSRGGVFRQGCTAFRVITPN	
rat	TALVAEYILTRKEAD-----	-LALQREPPVPFPYSHTSCQRKSRGGMFRQGCTAFRVITPN	
HC4	AALVAEFLHRKKL-----		FPNGCSAFKKITPN
HC1	AALIAEYILKRKG YWKVEKIC	TASLLSE DTHPCDSNSLLTTPSGGSMFSMGWPAFLSITPN	
HC3	AALVAEYILSMLED-----		RKYLPGVCVTFQNISSN
HC5	AALVAEYILSMLED-----		HSYLPVGSVSFQNISSN

		ITAM
HC2A	IDEEASM MEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAER YELIADIYKLIPI
KIAA	IDEEASM MEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAER YELIADIYKLIPI
rat	IDEEASM MEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP
HC4	IDEEGAMKEDAGMMD-----	VHYSEEV LLELLEQCVNGLWKAER YEITSEISKLI GPI
HC1	IKEEGA AKEDSGMHD-----	TPYNENILVEQLYMCGEFLWKSEYELIADVNKPIIAV
HC3	VLEESAVSDDV VSPDEEGICSGKYFTESGLVGLLEQAAASF	MAGMYEAVNEVYKVLIP I
HC5	VLEESV VSED T LSPDE DGVCAGQYFTESGLVGLLEQAAELF	STGGLYETVNEVYKLVIP I

	ITAM	ITAM	ITAM	ITAM
HC2A	YEKRRD-----			
KIAA	YEKRRD FERLAHL YDTIHRAYSKVTEVMHSGRRL LGTYFRV	AFFGQAAYQFTDSETDVE		
rat	SMKSGGTLETHLYDTIHRPYSKVTEVITR-----	A-----	AGSWDLLPGGLFGQ	
HC4	YENRREFENLTQVYRTIHGAYTKILEVMHTKKRLG-----		TFFRVAFY GQ	
HC1	FEKQRDFK KLS DLYDYD IHRSYLKVAEVVNSEKRLFG-----		FYYRVAFY GQ	
HC3	HEANRDAKKLSTIHGKLQEA FSKIVHQSTGWERMFG-----		TYFRVGFY G-	
HC5	LEAHREFRKLTLTHSKLQRA FDSIVNKH D--KRMFG-----		TYFRVGFFG-	

	ITAM	ITAM
HC2A	-FFEDEDGKEYIYKEPKLTPLSEISQRL LKLYSDRFGSENVKMIQDSGKVNPKDLDSKYA	
KIAA	GFFEDEDGKEYIYKEPKLTPLSEISQRL LKLYSDRFGSENVKMIQDSGKVNPKDLDSKYA	
rat	GFFEDEDGKEYIYKEPKLTPLSEISQRL LKLYSDRFGSENVKMIQDSGKVNPKDLDSKYA	
HC4	SFFEEDGKEYIYKEPKLTGLSEISLRLVKLYGERFGTENVKIIQSDSKVNAKELDPKYA	
HC1	GFFEEEGKEYIYKEPKLTGLSEISQRL LKLYADRF GADNVKIIQDSNKNVNPKDLDPKYA	
HC3	TKFGDLDEQEFVYKEPAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKA	
HC5	SKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGGCFGAEFVEVIK DSTPVDKTKLDPNKA	

	ITAM
HC2A	YIDVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA
KIAA	YIDVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA
rat	YIDVTHVIPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA
HC4	HIQVTVKPYFDDKELTERKTEFERHNISRFVFEAPYTL SGKKQGCIEEQCKRRTILT
HC1	YIQVTVVTPFFEEKEIEDRKTD FEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILT
HC3	YIQITYVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGEQFKRRTILT
HC5	YIQITFVEPYFDEYEMKDRVITYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLT



# Coiled-Coil 1

HC2A	IHC	FPYVKKRIPV	MYQHHTDLN	IEVAIDEMSKKVAELRQLC	SSAEVDMIKLQLKLQGSV
KIAA	IHC	FPYVKKRIPV	MYQHHTDLN	IEVAIDEMSKKVAELRQLC	SSAEVDMIKLQLKLQGSV
rat	IHC	FPYVKKRIPV	MYQHHTDLN	IEVAIDEMSKKVAELHQLC	SSAEVDMIKLQLKLQGSV
HC4	SNS	FPYVKKRIPIN	CEQQINLKE	IDGATDEIKDKTAELOKLC	SSTDVDMIQLQLKLQGSV
HC1	SHL	FPYVKKRIQVIS	QSSTELN	IEVAIDEMSRKVSELNQLCT	MEEVDMISLQLKLQGSV
HC3	SHAF	PIKTRVNVTHKEE	IILTR	IEVAIEDMQKKTQELAFATHQ	DPADPKMLQMVLOGSV
HC5	MHAF	PIKTRISVIQKEE	FVLTR	IEVAIEDMKKKTLQLAVAINQ	EPDAKMLQMVLOGSV

# Coiled-Coil 2

HC2A	SVQVNAGPLAYARAFLDDTNTKRYPD	NKVLLKEVFRQFVEACGQ	FLAVNERLIKEDQLE
KIAA	SVQVNAGPLAYARAFLDDTNTKRYPD	NKVLLKEVFRQFVEACGQ	FLAVNERLIKEDQLE
rat	SVQVNAGPLAYARAFLDDTNTKRYPD	NKVLLKEVFRQFVEACGQ	FLAVNERLIKEDQLE
HC4	SVQVNAGPLAYARAFLNDSQASKYPP	KKVSELKDMFRKFQACSIA	LELNERLIKEDQVE
HC1	SVKVNAGPMAYARAFLEETNAKKYP	DNQVKLLKEIFRQFADACGQ	LDVNERLIKEDQLE
HC3	GTTVNQGPLEVAQVFLSEIPSDPKL	FRHHNKLRLCFKDFTKRCED	ALRKNSLIGPVQKE
HC5	GATVNQGPLEVAQVFLAEIPADPKL	YRHHNKLRLCFKEFIMRCGEA	VEKNKRLITADQRE

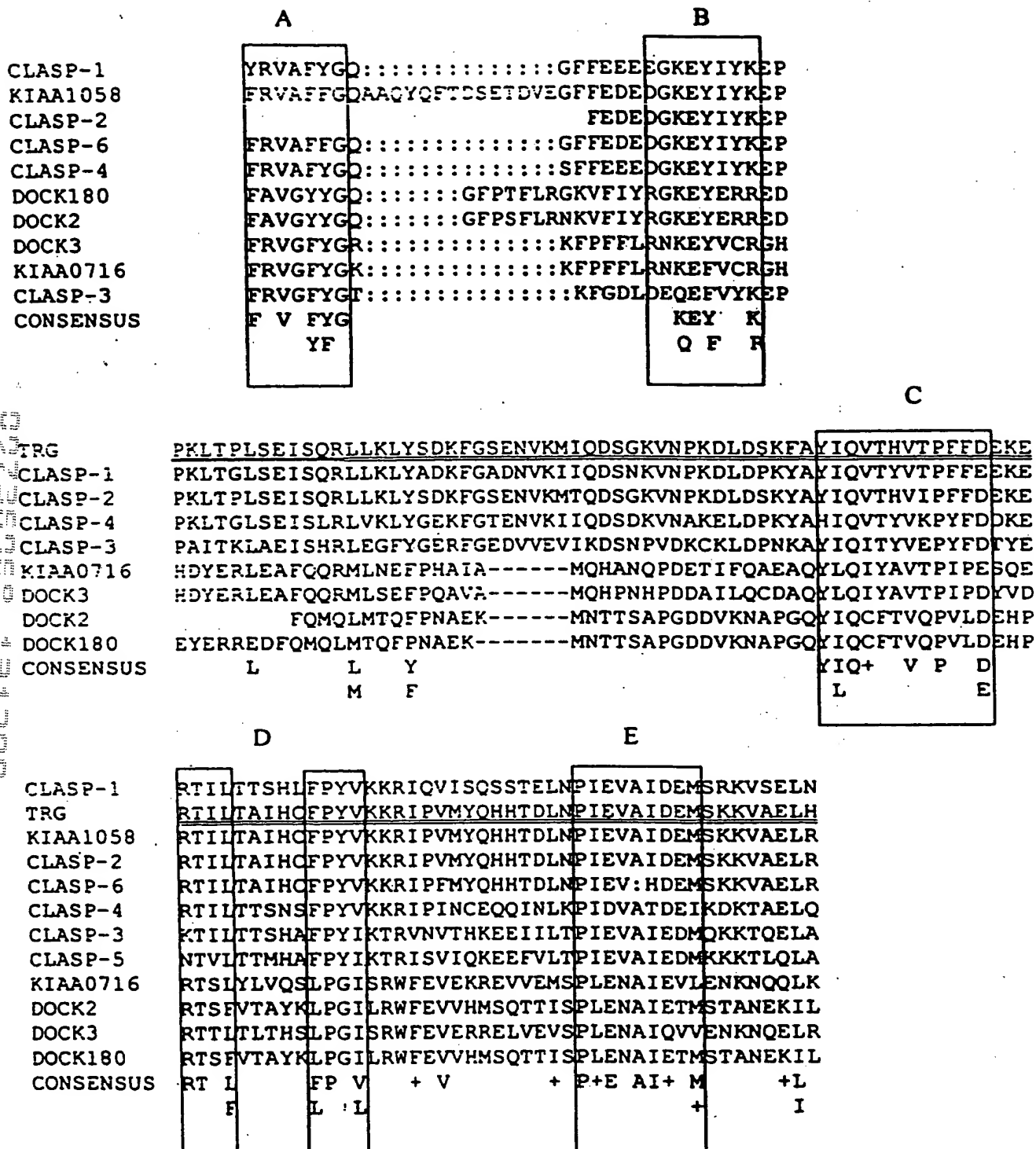
# Coiled-Coil 2

HC2A	YQEEMKANYREMAKELSEIMHE	QICPLEEKTS-VLPNSLHIFNAISGTPTSTMVHG	TSS
KIAA	YQEEMKANYREMAKELSEIMHE	QLG-----	
rat	YQEEMKANYREIRKELSDIIVER	ICPGEDKRATKFP	PAHLQRHORDTNKHSGSRVDQF
HC4	YHEGLKSNFRDMVKELSDIHE	QILOEDTMHSPWMSNTLHV	FCAISGTSSDRGYGSPRYA
HC1	YQEELRSHYKDMSELSTVMNE	QITGRDDLK---	RGVDQTCTRVISKATPALPTVS
HC3	YQRELG----	KLSS-----	PZ-----
HC5	YQOELKKNYNKLKENLRPMIER	KIPELYKPIFRVESQKRDSFHRSS	FRKCETQLSQGSZ-

# PRM

HC2A	SSVVZ-----
KIAA	-----
rat	-----
HC4	CVTLPHPEPHVGTCTFVMCKLR
HC1	TTFRANHWFCQAQEEAMNGREKE
HC3	PWTVIFNSRFYRSWGK
HC5	EVZ-----
	SAEVZ-----
	-----
	-----

HC2A	----
KIAA	----
rat	VHIFF
HC4	----
HC1	----
HC3	----
HC5	----



F

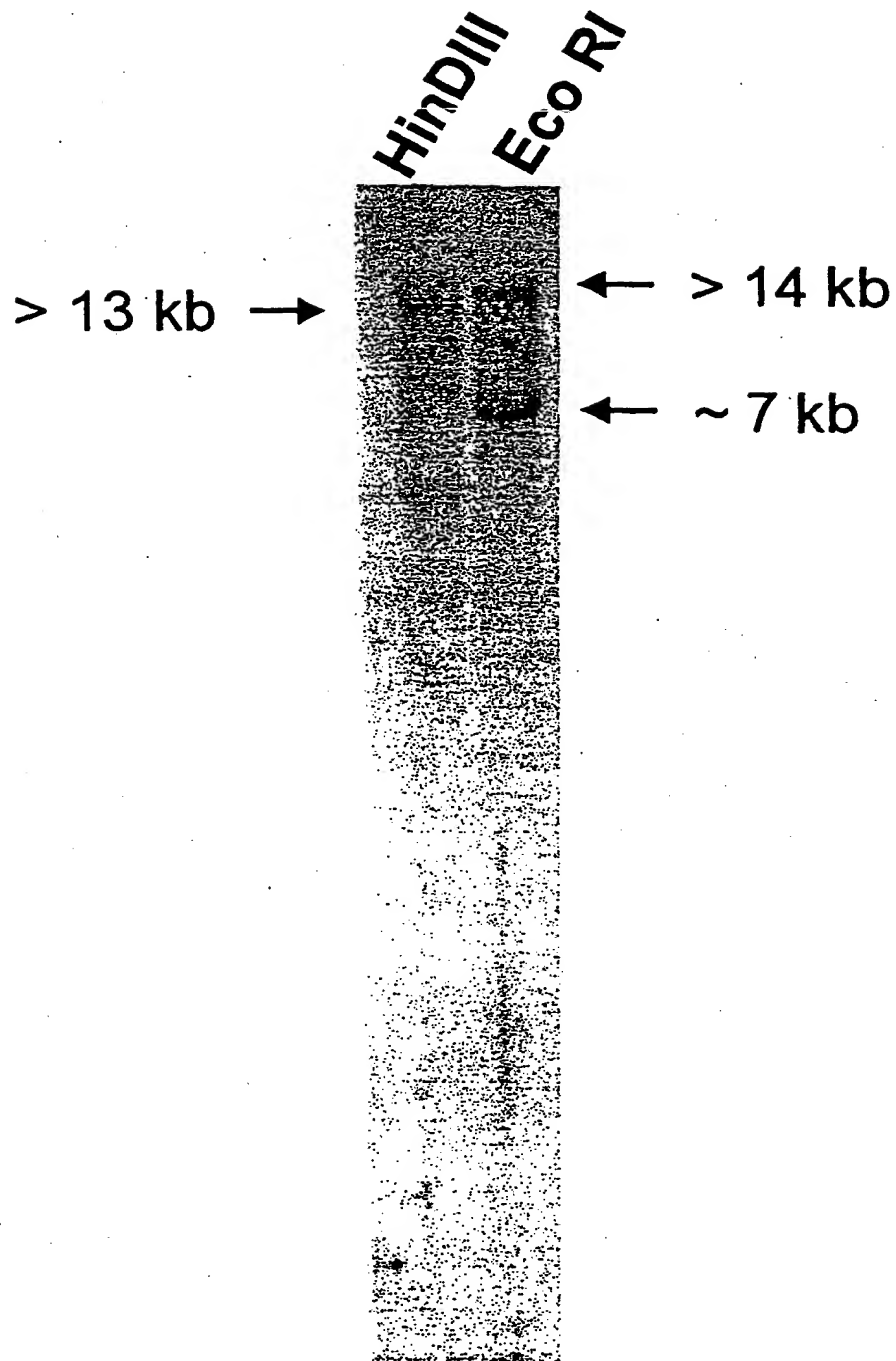
G

CLASP-1	SEQLKLOGSVSVKVNAG	PMAYARAFLEETNAKKY	PNQV--KLLKEIFRQFADACGQALD
TRG	KLQKLOGSVSVQVNAG	PLAYARAFLLDDTNTKRY	PNKV--KLLKEVFROFVEACGOALA
KIAA1056	KLQKLOGSVSVQVNAG	PLAYARAFLLDDTNTKRY	PNKV--KLLKEVFROFVEACGOALA
CLASP-2	KLQKLOGSVSVQVNAG	PLAYARAFLLDDTNTKRY	PNKV--KLLKEVFROFVEACGOALA
CLASP-6	KLQKLOGSVSVQVNAG	PLAYARAFLLDDTNTKRY	PNKV--KLLKEVFROFVEACGOALA
CLASP-3	MLQMVLOGSVGTTVNQG	LEVAQVFLSE--IPSDPKLFRHHNKLRLCFKDFTKRCEDALR	
CLASP-4	QLQKLOGCVSVQVNAG	PLAYARAFLLDSQASKYPPKKVSELKDMFRKFI--QACSI	ALE
CLASP-5	MLQMVLOGSVGATVNQG	LEVAQVFLAE--IPADPKLYRHHNKLRLCFKEFIMRCGEAVE	
KIAA0716	PLTMCLNGVIDAAVNGGV	SRVQEAFVKEYILSHPE	EDGEKIARLRELMLEQAQILEFGLA
DOCK2	PLSMLLNGIVDPAVMGG	FAKYEKAFFTEEYVRDHP	EDQDKLTHLKDLIAWQIPFLGAGIK
DOCK3	LLSMCLNGVIDAAVNGGI	ARYQEAFDKOYINKHP	GDAEKITQLKELMQEQVHVLGVGLA
DOCK180	PLSMLLNGIVDPAVMGG	FAKYEKAFFTEEYVRDHP	EAHEKIEKLKDLIAWQIPFLAEGIR
CONSENSUS	L M L+G V VN G	Y AFL + + P	L+
	L I	V V F +	I

DOCK1=KIAA0289

DOCK3=KIAA0299

CLASPvariant=KIAA1055



genomic DNA

FIG. 4

-12            -1  
GACGCGAGGACC

1/1	31/11
ATG GCT GCC TCC GAG CGC CGC GCC TTC GCG	CAC AAG ATC AAC AGG ACG GTG GCC GCA GAG
Met ala ala ser glu arg arg ala phe ala	his lys ile asn arg thr val ala ala glu
61/21	91/31
GTG CGG AAG CAG GTG TCC CGG GAA CGC AGT	GGC TCC CCC CAC TCC AGC AGG CGC TGC AGC
val arg lys gln val ser arg glu arg ser	gly ser pro his ser ser arg arg cys ser
121/41	151/51
AGC TCC CTG GGG GTC CCA CTG ACT GAA GTT	GTC GAG CCC CTG GAC TTT GAG GAT GTA CTT
ser ser leu gly val pro leu thr glu val	val glu pro leu asp phe glu asp val leu
181/61	211/71
CTG AGC CGG CCA CCA GAT GCT GAG CCC GGG	CCC CTC AGG GAC CTG GTA GAA TTC CCA GCT
leu ser arg pro pro asp ala glu pro gly	pro leu arg asp leu val glu phe pro ala
241/81	271/91
GAT GAC TTG GAG CTG CTG CTG CAG CCC CGG	GAA TGC CGG ACC ACG GAG CCC GGG ATC CCC
asp asp leu glu leu leu leu gln pro arg	glu cys arg thr thr glu pro gly ile pro
301/101	331/111
AAG GAT GAA AAA CTG GAT GCC CAG GTG AGG	GCC GCG GTG GAG ATG TAT ATT GAG GAC TGG
lys asp glu lys leu asp ala gln val arg	ala ala val glu met tyr ile glu asp trp
361/121	391/131
GTC ATT GTC CAC AGA AGG TAT CAG TAC CTG	AGT GCA GCA TAC AGC CCC GTC ACC ACA GAC
val ile val his arg arg tyr gln tyr leu	ser ala ala tyr ser pro val thr thr asp
421/141	451/151
ACA CAG CGG GAG CGA CAG AAG GGC CTC CCC	CGC CAG GTC TTT GAG CAG GAT GCT TCT GGA
thr gln arg glu arg gln lys gly leu pro	arg gln val phe glu gln asp ala ser gly
481/161	511/171
GAC GAG AGG TCC GGC CCT GAG GAC TCG AAT	GAC TCC CGG CGT GGC TCG GGC TCC CCG GAA
asp glu arg ser gly pro glu asp ser asn	asp ser arg arg gly ser gly ser pro glu
541/181	571/191
GAC ACC CCT CGA AGC AGT GGT GCC TCT AGC	ATC TTC GAC CTG AGG AAC CTG GCA GCT GAC
asp thr pro arg ser ser gly ala ser ser	ile phe asp leu arg asn leu ala ala asp
601/201	631/211
TCA TTG CTG CCC TCT CTG CTA GAG CGG GCG	GCC CCA GAA GAT GTG GAC CGG CGC AAT GAA
ser leu leu pro ser leu leu glu arg ala	ala pro glu asp val asp arg arg asn glu
661/221	691/231
ACC CTT CGA CGG CAG CAC CGG CCC CCG GCC	CTG CTC ACC CTC TAC CCG GCA CCT GAC GAG
thr leu arg arg gln his arg pro pro ala	leu leu thr leu tyr pro ala pro asp glu
721/241	751/251
GAT GAA GCC GTG GAA CGC TGT AGC CGC CCA	GAG CCA CCC CGC GAG CAC TTT GGA CAA AGG
asp glu ala val glu arg cys ser arg pro	glu pro pro arg glu his phe gly gln arg
781/261	811/271
ATC TTG GTC AAG TGT CTG TCG CTC AAG TTC	GAG ATT GAA ATT GAG CCC ATC TTT GGG ATC
ile leu val lys cys leu ser leu lys phe	glu ile glu ile glu pro ile phe gly ile
841/281	871/291
TTG GCT CTG TAT GAT GTG CGG GAG AAA AAG	AAG ATC TCG GAG AAC TTC TAC TTC GAC CTG
leu ala leu tyr asp val arg glu lys lys	lys ile ser glu asn phe tyr phe asp leu
901/301	931/311
AAC TCG GAC TCC ATG AAG GGG CTG CTT CGG	GCT CAT GGC ACC CAC CCT GCC ATC TCC ACC
asn ser asp ser met lys gly leu leu arg	ala his gly thr his pro ala ile ser thr
961/321	991/331
CTG GCC CGC TCT GCC ATC TTC TCT GTG ACC	TAC CCC TCA CCT GAC ATC TTC CTG GTC ATC
leu ala arg ser ala ile phe ser val thr	tyr pro ser pro asp ile phe leu val ile
1021/341	1051/351
AAG TTG GAG AAG GTG CTT CAG CAA GGG GAC	ATC AGT GAG TGC TGT GAG CCT TAC ATG GTG
lys leu glu lys val leu gln gln gly asp	ile ser glu cys cys glu pro tyr met val
1081/361	1111/371

TTG AAA GAA GTG GAC ACA GCC AAG AAC AAA GAG AAG CTA GAG AAG CTG CGC CTG GCG GCC  
 leu lys glu val asp thr ala lys asn lys glu lys leu glu lys leu arg leu ala ala  
 1141/381 1171/391  
 GAG CAG TTC TGC ACC CGC CTG GGC CGC TAC CGC ATG CCC TTC GCC TGG ACG GCC GTG CAC  
 glu gln phe cys thr arg leu gly arg tyr arg met pro phe ala trp thr ala val his  
 1201/401 1231/411  
 TTG GCC AAC ATC GTG AGC AGC GCT GGG CAG CTG GAC CGG GAC TCT GAC TCG GAG GGC GAG  
 leu ala asn ile val ser ser ala gly gln leu asp arg asp ser asp ser glu gly glu  
 1261/421 1291/431  
 CGC CGG CCA GCC TGG ACA GAC CGC CGC CGT CGG GGG CCC CAG GAC CGG GCG AGT AGT GGG  
 arg arg pro ala trp thr asp arg arg arg arg gly pro gln asp arg ala ser ser gly  
 1321/441 1351/451  
 GAC GAC GCC TGC AGC TTC TCT GGC TTC CGT CCA GCC ACG CTA ACT GTC ACA AAC TTC TTT  
 asp asp ala cys ser phe ser gly phe arg pro ala thr leu thr val thr asn phe phe  
 1381/461 1411/471  
 AAG CAG GAG GCT GAG CGA CTC AGT GAC GAG GAC CTC TTC AAG TTC CTG GCT GAC ATG AGG  
 lys gln glu ala glu arg leu ser asp glu asp leu phe lys phe leu ala asp met arg  
 1441/481 1471/491  
 CGC CCG TCG TCC CTG CTG CGG CGA CTA CGT CCT GTG ACT GCC CAG CTC AAG ATC GAC ATT  
 arg pro ser ser leu leu arg arg leu arg pro val thr ala gln leu lys ile asp ile  
 1501/501 1531/511  
 TCT CCG GCT CCT GAA AAT CCC CAC TTC TGC CTC TCC CCT GAG CTG CTT CAT ATC AAG CCC  
 ser pro ala pro glu asn pro his phe cys leu ser pro glu leu leu his ile lys pro  
 1561/521 1591/531  
 TAC CCG GAC CCC AGG GGC CGG CCC ACC AAG GAG ATT CTG GAG TTC CCC GCC CGC GAA GTC  
 tyr pro asp pro arg gly arg pro thr lys glu ile leu glu phe pro ala arg glu val  
 1621/541 1651/551  
 TAT GCC CCC CAT ACC AGC TAC AGG AAC CTG CTG TAC GTG TAC CCG CAC AGC CTC AAC TTC  
 tyr ala pro his thr ser tyr arg asn leu leu tyr val tyr pro his ser leu asn phe  
 1681/561 1711/571  
 AGC AGC CGC CAG GGC TCC GTG CGC AAC CTT GCT GTG CGA GTG CAG TAC ATG ACA GGC GAG  
 ser ser arg gln gly ser val arg asn leu ala val arg val gln tyr met thr gly glu  
 1741/581 1771/591  
 GAC CCC AGC CAG GCT CTG CCG GTC ATC TTT GGC AAG TCC AGC TGC AGT GAA TTT ACC CGC  
 asp pro ser gln ala leu pro val ile phe gly lys ser ser cys ser glu phe thr arg  
 1801/601 1831/611  
 GAG GCC TTC ACA CCG GTG GTC TAC CAT AAC AAG TCC CCC GAG TTC TAC GAG GAG TTC AAG  
 glu ala phe thr pro val val tyr his asn lys ser pro glu phe tyr glu glu phe lys  
 1861/621 1891/631  
 CTG CAT CTT CCA GCC TGC GTG ACA GAG AAC CAT CAC CTG CTG TTC ACC TTC TAC CAT GTC  
 leu his leu pro ala cys val thr glu asn his his leu leu phe thr phe tyr his val  
 1921/641 1951/651  
 AGC TGC CAG CCC CGG CCG GGC ACT GCC CTG GAG ACA CCC GTG GGC TTT ACT TGG ATC CCA  
 ser cys gln pro arg pro gly thr ala leu glu thr pro val gly phe thr trp ile pro  
 1981/661 2011/671  
 CTG CTG CAG CAC GGG CGC CTG AGG ACC GGC CCC TTC TGT CTC CCA GTG TCT GTG GAC CAG  
 leu leu gln his gly arg leu arg thr gly pro phe cys leu pro val ser val asp gln  
 2041/681 2071/691  
 CCG CCG CCC AGC TAT TCC GTG CTC ACA CCC GAT GTG GCG CTT CCG GGC ATG CGC TGG GTG  
 pro pro pro ser tyr ser val leu thr pro asp val ala leu pro gly met arg trp val  
 2101/701 2131/711  
 GAC GGT CAC AAG GGC GTG TTC AGT GTG GAG CTC ACA GCC GTG TCC TCT GTG CAC CCC CAG  
 asp gly his lys gly val phe ser val glu leu thr ala val ser ser val his pro gln  
 2161/721 2191/731  
 GAC CCC TAC CTG GAC AAA TTC TTC ACC CTG GTG CAC GTC CTG GAG GAG GGA GCC TTC CCA  
 asp pro tyr leu asp lys phe phe thr leu val his val leu glu glu gly ala phe pro  
 2221/741 2251/751  
 TTC CGG CTC AAG GAC ACT GTG CTG AGC GAG GGC AAC GTG GAG CAG GAG CTG CGG GCC AGT  
 phe arg leu lys asp thr val leu ser glu gly asn val glu gln glu leu arg ala ser  
 2281/761 2311/771  
 CTT GCA GCA CTG CGC CTG GCC AGC CCC GAA CCC CTT GTG GCC TTC TCC CAC CAC GTG CTG

leu ala ala leu arg leu ala ser pro glu pro leu val ala phe ser his his val leu  
 2341/781 2371/791  
 GAC AAG CTC GTG CGT CTG GTC ATC AGG CCC CCG ATC ATC AGT GGC CAG ATT GTG AAC CTG  
 asp lys leu val arg leu val ile arg pro pro ile ile ser gly gln ile val asn leu  
 2401/901 2431/811  
 GGC CGT GGA GCC TTT GAA GCA ATG GCC CAT GTA GTC AGC CTT GTT CAC CGG AGC CTG GAG  
 gly arg gly ala phe glu ala met ala his val val ser leu val his arg ser leu glu  
 2461/821 2491/831  
 GCA GCC CAG GAT GCC CGC GGT CAC TGC CCA CAG CTG GCT GCC TAC GTC CAC TAC GCC TTT  
 ala ala gln asp ala arg gly his cys pro gln leu ala ala tyr val his tyr ala phe  
 2521/841 2551/851  
 CGC CTT CCT GGC ACT GAG CCC AGC CTC CCG GAT GGG GCC CCT CCA GTG ACA GTG CAG GCT  
 arg leu pro gly thr glu pro ser leu pro asp gly ala pro pro val thr val gln ala  
 2581/861 2611/871  
 GCC ACA CTG GCC CGT GGC TCT GGT CGC CCC GCA AGC CTC TAC CTG GCG CGT TCC AAG AGC  
 ala thr leu ala arg gly ser gly arg pro ala ser leu tyr leu ala arg ser lys ser  
 2641/881 2671/891  
 ATC AGC AGC AGC AAC CCT GAC CTC GCC GTG GCC CCT GGC TCT GTG GAT GAC GAG GTT TCC  
 ile ser ser ser asn pro asp leu ala val ala pro gly ser val asp asp glu val ser  
 2701/901 2731/911  
 CGC ATC CTG GCC AGC AAG CTG CTT CAC GAG GAG CTG GCT CTG CAG TGG GTG GTC AGC AGC  
 arg ile leu ala ser lys leu leu his glu glu leu ala leu gln trp val val ser ser  
 2761/921 2791/931  
 AGT GCC GTA CGC GAG GCC ATC CTC CAG CAC GCC TGG TTC TTC TTC CAG CTC ATG GTG AAG  
 ser ala val arg glu ala ile leu gln his ala trp phe phe phe gln leu met val lys  
 2821/941 2851/951  
 AGT ATG GCG CTG CAC CTG CTG CTT GGC CAG CGA CTA GAC ACA CCC CGC AAG CTG CGC TTC  
 ser met ala leu his leu leu leu gly gln arg leu asp thr pro arg lys leu arg phe  
 2881/961 2911/971  
 CCC GGA CGC TTC CTG GAC GAC ATC ACT GCC TTG GTG GGC TCT GTG GGC CTG GAG GTC ATC  
 pro gly arg phe leu asp asp ile thr ala leu val gly ser val gly leu glu val ile  
 2941/981 2971/991  
 ACC CGT GTC CAC AAG GAT GTG GAG CTG GCC GAG CAC CTC AAC GCC AGC CTG GCT TTC TTC  
 thr arg val his lys asp val glu leu ala glu his leu asn ala ser leu ala phe phe  
 3001/1001 3031/1011  
 CTC AGT GAC CTT CTG TCC CTG GTG GAC CGG GGC TTT GTC TTC AGC CTG GTC CGG GCC CAC  
 leu ser asp leu leu ser leu val asp arg gly phe val phe ser leu val arg ala his  
 3061/1021 3091/1031  
 TAC AAG CAG GTG GCC ACG CGG CTC CAG TCG TCC CCT AAT CCA GCA GCC CTG CTG ACC CTG  
 tyr lys gln val ala thr arg leu gln ser ser pro asn pro ala ala leu leu thr leu  
 3121/1041 3151/1051  
 CGC ATG GAA TTC ACC CGC ATC CTG TGC AGC CAC GAG CAC TAC GTG ACC CTC AAC CTC CCC  
 arg met glu phe thr arg ile leu cys ser his glu his tyr val thr leu asn leu pro  
 3181/1061 3211/1071  
 TGC TGC CCC CTG TCA CCT CCA GCC TCG CCC TCC CCC TCT GTG TCC TCC ACC ACC TCC CAG  
 cys cys pro leu ser pro pro ala ser pro ser pro ser val ser ser thr thr ser gln  
 3241/1081 3271/1091  
 AGC TCC ACC TTC TCC AGC CAA GCC CCG GAC CCC AAG GTG ACC AGC ATG TTC GAA CTG AGT  
 ser ser thr phe ser ser gln ala pro asp pro lys val thr ser met phe glu leu ser  
 3301/1101 3331/1111  
 GGA CCA TTC CGG CAG CAG CAC TTC CTA GCT GGG CTC CTG CTG ACG GAG CTG GCA CTG GCC  
 gly pro phe arg gln gln his phe leu ala gly leu leu leu thr glu leu ala leu ala  
 3361/1121 3391/1131  
 CTC GAA CCT GAG GCT GAA GGG GCA TTC CTG TTG CAC AAG AAG GCC ATC AGT GCT GTG CAC  
 leu glu pro glu ala glu gly ala phe leu leu his lys lys ala ile ser ala val his  
 3421/1141 3451/1151  
 AGC CTG CTA TGT GGC CAT GAC ACT GAC CCC CGC TAC GCC GAG GCC ACT GTG AAG GCT CGT  
 ser leu leu cys gly his asp thr asp pro arg tyr ala glu ala thr val lys ala arg  
 3481/1161 3511/1171  
 GTG GCC GAG CTG TAC CTG CCA CTG CTT TCG ATT GCA CGG GAT ACC TTG CCA CGG CTG CAT  
 val ala glu leu tyr leu pro leu leu ser ile ala arg asp thr leu pro arg leu his

3541/1181	GAC TTT GCT GAG GGC CCA GGT CAG CGG TCA	3571/1191	AGA CTG GCC TCA ATG CTT GAC TCA GAC ACA
asp phe ala glu gly pro gly gln arg ser		arg leu ala ser met leu asp ser asp thr	
3601/1201	GAA GGC GAA GGG GAC ATT GCG GGT ACC ATC	3631/1211	AAC CCC TCT GTG GCC ATG GCC ATT GCT GGT
glu gly glu gly asp ile ala gly thr ile		asn pro ser val ala met ala ile ala gly	
3661/1221	GGC CCC CTA GCC CCT GGC TCC CGG GCC AGC	3691/1231	ATC TCC CAG GGG CCA CCA ACG GCT TCT CGC
gly pro leu ala pro gly ser arg ala ser		ile ser gln gly pro pro thr ala ser arg	
3721/1241	GCA GGC TGT GCC CTC TCT GCT GAG TCA AGC	3751/1251	CGG ACC TTG CTG GCG TGT GTG CTG TGG GTG
ala gly cys ala leu ser ala glu ser ser		arg thr leu leu ala cys val leu trp val	
3781/1261	CTG AAA AAC ACC GAG CCG GCG CTC CTG CAG	3811/1271	CGC TGG GCC ACT GAC CTG ACA CTC CCC CAG
leu lys asn thr glu pro ala leu leu gln		arg trp ala thr asp leu thr leu pro gln	
3841/1281	CTG GGA CGT CTG TTG GAC TTG CTG TAC CTT	3871/1291	TGC CTG GCT GCC TTT GAG TAC AAG GGG AAA
leu gly arg leu leu asp leu leu tyr leu		cys leu ala ala phe glu tyr lys gly lys	
3901/1301	AAG GCC TTT GAA CGC ATC AAC AGC CTC ACA	3931/1311	TTC AAA AAA TCT CTG GAT ATG AAG GCG CGG
lys ala phe glu arg ile asn ser leu thr		phe lys lys ser leu asp met lys ala arg	
3961/1321	CTA GAG GAA GCC ATT CTG GGT ACC ATC GGA	3991/1331	GCT CGA CAA GAA ATG GTT CGG CGA AGT CGT
leu glu glu ala ile leu gly thr ile gly		ala arg gln glu met val arg arg ser arg	
4021/1341	GAG AGG AGC CCG TTT GGG AAT CCA GAG AAC	4051/1351	GTG CGC TGG CGG AAG AGC GTC ACA CAC TGG
glu arg ser pro phe gly asn pro glu asn		val arg trp arg lys ser val thr his trp	
4081/1361	AAG CAA ACC TCA GAC CGC GTG GAC AAG ACC	4111/1371	AAG GAT GAA ATG GAA CAC GAG GCC TTG GTG
lys gln thr ser asp arg val asp lys thr		lys asp glu met glu his glu ala leu val	
4141/1381	GAA GGG AAC CTG GCA ACC GAG GCA AGC CTA	4171/1391	GTG GTT CTG GAC ACA CTG GAG ATC ATC GTG
glu gly asn leu ala thr glu ala ser leu		val val leu asp thr leu glu ile ile val	
4201/1401	CAG ACG GTG ATG CTT TCA GAA GCC CGG GAG	4231/1411	AGC GTC TTG GGG GCA GTG CTG AAG GTT GTG
gln thr val met leu ser glu ala arg glu		ser val leu gly ala val leu lys val val	
4261/1421	CTG TAC AGC CTG GGC AGT GCC CAG AGT GCC	4291/1431	CTC TTC TTG CAG CAT GGC CTG GCC ACC CAG
leu tyr ser leu gly ser ala gln ser ala		leu phe leu gln his gly leu ala thr gln	
4321/1441	AGG GCC CTT GTG TCC AAG TTC CCG GAG CTG	4351/1451	CTG TTC GAG GAG GAC ACG GAG CTG TGT GCC
arg ala leu val ser lys phe pro glu leu		leu phe glu glu asp thr glu leu cys ala	
4381/1461	GAC CTG TGC CTG AGG CTC CTA CGA CAC TGT	4411/1471	GCG AGC CGC ATC AGC ACC ATC CGC ACG CAC
asp leu cys leu arg leu leu arg his cys		gly ser arg ile ser thr ile arg thr his	
4441/1481	GCC AGC GCC TCG CTG TAC CTG CTC ATG CGA	4471/1491	CAG AAC TTC GAG ATC GGC CAC AAC TTT GCC
ala ser ala ser leu tyr leu leu met arg		gln asn phe glu ile gly his asn phe ala	
4501/1501	CGT GTG AAG ATG CAG GTC ACC ATG TCT CTC	4531/1511	TCG TCC CTG GTG GGG ACG ACG CAG AAC TTC
arg val lys met gln val thr met ser leu		ser ser leu val gly thr thr gln asn phe	
4561/1521	AGT GAA GAG CAC CTG CGA CGT TCA CTC AAA	4591/1531	ACC ATC CTC ACC TAT GCT GAG GAG GAC ATG
ser glu glu his leu arg arg ser leu lys		thr ile leu thr tyr ala glu glu asp met	
4621/1541	GGG CTG CGG GAC AGC ACC TTC GCA GAG CAG	4651/1551	GTC CAG GAC CTG ATG TTC AAC CTG CAC ATG
gly leu arg asp ser thr phe ala glu gln		val gln asp leu met phe asn leu his met	
4681/1561	ATC CTG ACG GAC ACG GTG AAG ATG AAG GAA	4711/1571	CAC CAG GAG GAC CCT GAG ATG CTC ATC GAC
ile leu thr asp thr val lys met lys glu		his gln glu asp pro glu met leu ile asp	
4741/1581		4771/1591	



CTC ATG TAC AGA ATT GCC CGG GGC TAC CAG GGC TCA CCG GAC CTT CGG CTG ACC TGG TTG  
 leu met tyr arg ile ala arg gly tyr gln gly ser pro asp leu arg leu thr trp leu  
 4801/1601 4831/1611  
 CAG AAC ATG GCC GGG AAG CAC GCG GAG CTG GGC AAC CAC GCC GAG GCC GCC CAG TGC ATG  
 gln asn met ala gly lys his ala glu leu gly asn his ala glu ala ala gln cys met  
 4861/1621 4891/1631  
 GTG CAC GCG GCC GCC CTC GTG GCT GAG TAC CTC GCC CTG CTC GAG GAC CAG CGC CAC CTG  
 val his ala ala ala leu val ala glu tyr leu ala leu leu glu asp gln arg his leu  
 4921/1641 4951/1651  
 CCC GTG GGC TGC GTT TCC TTC CAG AAC ATC TCA TCC AAC GTG CTA GAG GAG TCC GCC ATC  
 pro val gly cys val ser phe gln asn ile ser ser asn val leu glu glu ser ala ile  
 4981/1661 5011/1671  
 TCC GAC GAC ATC CTG TCG CCC GAC GAG GAG GGC TTC TGC TCC GGG AAG CAC TTC ACT GAG  
 ser asp asp ile leu ser pro asp glu glu gly phe cys ser gly lys his phe thr glu  
 5041/1681 5071/1691  
 CTG GGG CTG GTA GGG TTG CTG GAA CAG GCA GCC GGC TAC TTC ACC ATG GGC GGG CTC TAC  
 leu gly leu val gly leu leu glu gln ala ala gly tyr phe thr met gly gly leu tyr  
 5101/1701 5131/1711  
 GAG GCG GTG AAT GAG GTC TAC AAG AAC CTC ATC CCC ATC CTG GAA GCC CAC CGT GAC TAC  
 glu ala val asn glu val tyr lys asn leu ile pro ile leu glu ala his arg asp tyr  
 5161/1721 5191/1731  
 AAG AAG CTG GCC GCG GTG CAC GGC AAA CTG CAG GAG GCC TTC ACC AAG ATC ATG CAC CAG  
 lys lys leu ala ala val his gly lys leu gln glu ala phe thr lys ile met his gln  
 5221/1741 5251/1751  
 AGT TCC GGC TGG GAG CGC GTG TTC GGG ACG TAT TTC CGC GTG GGC TTC TAC GGC GCC CAC  
 ser ser gly trp glu arg val phe gly thr tyr phe arg val gly phe tyr gly ala his  
 5281/1761 5311/1771  
 TTC GGT GAC CTG GAT GAG CAG GAG TTT GTG TAC AAG GAG CCA TCG ATC ACG AAG CTG GCA  
 phe gly asp leu asp glu gln glu phe val tyr lys glu pro ser ile thr lys leu ala  
 5341/1781 5371/1791  
 GAG ATC TCA CAC CGG CTG GAG GAG TTC TAC ACG GAG AGA TTT GGC GAC GAC GTC GTT GAG  
 glu ile ser his arg leu glu glu phe tyr thr glu arg phe gly asp asp val val glu  
 5401/1801 5431/1811  
 ATT ATC AAA GAC TCT TAC CCT GTG GAC AAG TCC AAG CTT GAC TCA CAA AAG GCC TAC ATC  
 ile ile lys asp ser tyr pro val asp lys ser lys leu asp ser gln lys ala tyr ile  
 5461/1821 5491/1831  
 CAG ATC ACG TAT GTG GAA CCG TAC TTT GAT ACC TAC GAG CTC AAG GAC CGG GTG ACC TAC  
 gln ile thr tyr val glu pro tyr phe asp thr tyr glu leu lys asp arg val thr tyr  
 5521/1841 5551/1851  
 TTT GAC CGC AAC TAT GGG CTT CGC ACA TTC CTG TTC TGC ACG CCG TTC ACG CCG GAT GGG  
 phe asp arg asn tyr gly leu arg thr phe leu phe cys thr pro phe thr pro asp gly  
 5581/1861 5611/1871  
 CGC GCA CAC GGG GAG CTG CCC GAG CAA CAC AAG CGT AAG ACG CTG CTC AGC ACC GAC CAC  
 arg ala his gly glu leu pro glu gln his lys arg lys thr leu leu ser thr asp his  
 5641/1881 5671/1891  
 GCC TTC CCC TAC ATC AAG ACT CGC ATC CGT GTG TGC CAC CGG GAG GAG ACG GTG CTG ACG  
 ala phe pro tyr ile lys thr arg ile arg val cys his arg glu glu thr val leu thr  
 5701/1901 5731/1911  
 CCA GTG GAG GTG GCC ATC GAG GAC ATG CAG AAG AAG ACA CGG GAG CTG GCC TTT GCC ACC  
 pro val glu val ala ile glu asp met gln lys lys thr arg glu leu ala phe ala thr  
 5761/1921 5791/1931  
 GAG CAG GAC CCA CCA GAT GCT AAG ATG CTA CAG ATG GTG CTT CAG GGC TCT GTA GGG CCC  
 glu gln asp pro pro asp ala lys met leu gln met val leu gln gly ser val gly pro  
 5821/1941 5851/1951  
 ACC GTG AAC CAG GGT CCC CTG GAG GTG GCC CAG GTG TTT TTA GCA GAG ATC CCG GAA GAC  
 thr val asn gln gly pro leu glu val ala gln val phe leu ala glu ile pro glu asp  
 5881/1961 5911/1971  
 CCC AAG CTC TTC CGG CAT CAC AAC AAA TTG CGG CTC TGC TTC AAG GAC TTC TGC AAG AAA  
 pro lys leu phe arg his his asn lys leu arg leu cys phe lys asp phe cys lys lys  
 5941/1981 5971/1991  
 TGT GAG GAT GCG CTG CGG AAA AAT AAG GCC CTG ATT GGG CCG GAC CAG AAG GAG TAC CAC

cys glu asp ala leu arg lys asn lys ala leu ile gly pro asp gln lys glu tyr his  
 6001/2001 6031/2011  
 CGT GAG CTG GAG CGC AAC TAC TGC CGC CTG CGG GAG GCT CTG CAG CCC CTG CTT ACC CAG  
 arg glu leu glu arg asn tyr cys arg leu arg glu ala leu gln pro leu leu thr gln  
 6061/2021 6091/2031  
 CGC CTG CCC CAG CTG ATG GCA CCC ACC CCA CCC GGC CTC AGG AAC TCC TTG AAC AGA GCA  
 arg leu pro gln leu met ala pro thr pro pro gly leu arg asn ser leu asn arg ala  
 6121/2041 6151/2051  
 AGT TTC CGA AAG GCA GAC CTC TGA GCC CAC AAG GAC CAA AGC TGT ACC TAG AGG AAC CAG  
 ser phe arg lys ala asp leu OPA  
 6181/2061 6211/2071  
 CAC CCG GGC CTC AGC TGT CTG TGC TGC GAG GGG AGT CTG CCC TGG TGC CCA CTG GGC TGT  
  
 6241/2081 6271/2091  
 GGG GTG ACC ACA CTG TAC TTG GGG CTG GGC CCT CTG CCC CTG TGT CCC CAT CTG TGT GCA  
  
 6301/2101 6331/2111  
 CTG ATG CTT CCT CCC TTT TTT AAT TTA AAA TGG TTT TTA TAA GCA AAA AAA AAA AAA AAA

**A. Allelic variations: single nucleotide changes (polymorphism) between CLASP-7 cDNA isoforms**

Isoform	Nucleotide(s)	Consequence
1	1993	G to A; glycine to arginine
2	2136	A to G; missense
3	3166	A to G; threonine to alanine
4	3902	A to T; lysine to methionine
5	3918	C to T; missense
6	3937	A to C; lysine to glutamine
7	4002	A to C; glutamic acid to aspartic acid
8	4017	T to A; serine to arginine
9	4020	T to C; missense
10	4034-5	TT to AC; phenylalanine to tyrosine
11	4911	G to C change; missense mutation changing codon from glutamine to histidine

These differences may be found separately or together in various combination in the difference human CLASP-7 isoforms

FIG. 5

**B**

C

FIG. 5

CLASP-7 intron/exons

Exon 63800 to 63920

GCGGGGCGGGGCCCCGGGGCGGCGGGCGGGACGCGAGGACCATGGCTGC  
CTCCGAGCGCCGCGCCTTCGCGCACAAAGATCAACAGGTAGTGTGGCCGCGGG  
GCCCCCTCCACCTCCC

Exon 72530 to 72670

CCAATGGCCCCCTCCCTATCTTTCCAGGACGGTGGCCGCAGAGGTGCGGAAG  
CAGGTGTCCCGGGAACGCAGTGGCTCCCCCCTCCAGCAGGCGCTGCAGCA  
GCTCCCTGGGGGTAAAGTATTTGGGGGTCCGCCCCCA

Exon 73300 to 73530

TCACAGCCACTTTGCTCCAATCCAGGTCCCACTGACTGAAGTTGTCGAGCCCC  
TGGACTTTGAGGATGTACTTCTGAGCCGGCCACCAGATGCTGAGCCCCGGGCC  
CCTCAGGGACCTGGTAGAATTCCCAGCTGATGACTTGGAGCTGCTGCTGCAG  
CCCCGGGAATGCCGGACCACGGAGCCCCGGGATCCCCAAGGATGAGTGGGTTC  
AGCCCCACGCCCTCTCTGCCTG

Exon 73700 to 73830

GTCTCTGTTTACCCTGATCTTCTTTTGCTGCAGAAACTGGATGCCCAGGTGA  
GGGCCGCGGTGGAGATGTATATTGAGGACTGGGTCATTGTCCACAGAAGGTG  
AGTCTGACTTAGGGGCAGCTCAGGGG

Exon 74010 to 74190

CCTGCCCAGCCCCGTTTCCTGCTAGGTATCAGTACCTGAGTGCAGCATAACAGC  
CCCGTCACCACAGACACACAGCGGGAGCGACAGAAGGGCCTCCCCCGCCAG  
GTCTTTGAGCAGGATGCTTCTGGAGACGAGAGGTCCGGCCCTGAGGACTCGG  
TGAGGAAGCCCCTGGCTGGGGTCAC

Exon 75170 to 75450

CAGTGCTTGACATTCTCCACTGGCAGAAATGACTCCCGGCGTGGCTCGGGCTC  
CCCGGAAGACACCCCTCGAAGCAGTGGTGCCTCTAGCATCTTCGACCTGAGG  
AACCTGGCAGCTGACTCATTGCTGCCCTCTCTGCTAGAGCGGGCGGCCCCAG  
AAGATGTGGACCGGCGCAATGAAACCCTTCGACGGCAGCACCGGCCCCCGGC  
CCTGCTCACCCCTCTACCCGGCACCTGACGAGGTGGGTGCCCTTCCCAGATAT  
CAGCCAACCAGCATTACT

Exon 78100 to 78250

CCCGCCCAGCTCCCACCCCCCACTCTTGGCAGGATGAAGCCGTGGAACGCTG  
TAGCCGCCAGAGCCACCCCGCGAGCACTTTGGACAAAGGATCTTGGTCAAG  
TGTCTGTCGCTCAAGTGAGTATACTGACATGTCTCTCTTCTTAGATG

Exon 80380 to 80500

CCCCCTCCCTCCCATTACTTGTAGGTTTCGAGATTGAAATTGAGCCCATCTTT  
GGGATCTTGGCTCTGTATGATGTGCGGGAGAAAAAGAAGGTAGGAGGCCCTT  
TTTTCTCTTTCCTCCC

Exon 80540 to 80750

GTGGTGGCCCAGCTGCCTCTGGTGTCCCCAGATCTCGGAGAACTTCTACTTCG  
ACCTGAACTCGGACTCCATGAAGGGGCTGCTTCGGGCTCATGGCACCCACCC  
TGCCATCTCCACCCTGGCCCGCTCTGCCATCTTCTCTGTGACCTACCCCTCACC  
TGACATCTTCCTGGTCATCAAGGTGCCTGCTGGGGCTGGGCAAGGGGGTGGT

Exon 82370 to 82510

GCCTCACTGGATTCATTCATCTGCCCCGCAGTTGGAGAAGGTGCTTCAGCAAG  
GGGACATCAGTGAGTGCTGTGAGCCTTACATGGTGTGAAAGAAGTGGACAC  
AGCCAAGGTAAGCGTGTGGAGGCTGGACTAGGGGCA

Exon 82540 to 82760

GCTGAGCTGGCAGGGGACGGGGTCTCCCCACAGAACAAAGAGAAGCTAGAG  
AAGCTGCGCCTGGCGGGCCGAGCAGTTCTGCACCCGCGCTGGGCCGCTACCGCA  
TGCCCTTCGCCTGGACGGCCGTGCACTTGGCCAACATCGTGAGCAGCGCTGG  
GCAGCTGGACCGGGACTCTGACTCGGAGGGGCGGTGAGGAGGCGGGGGCTAAC  
AGGCTTGGGGCGGGG

Exon 82860 to 83060

CTTGGTCCCCCTTTTGTCAATTGTCATTCCCTCCCCTAGAGCGCCGGCCAGCCT  
GGACAGACCGCCGCGGTCGGGGGCCCCAGGACCGGGCGAGTAGTGGGGACG  
ACGCCTGCAGCTTCTCTGGCTTCCGTCCAGCCACGCTAACTGTCACAACTTC  
TTTAAGCAGGTGTCCTACCCTGGGGCCAGGGACTCTCCCACTCC

Exon 83100 to 83260

GCCCAGGCTGACGGGAGTGGGTCCCATGTAGGAGGCTGAGCGACTCAGTGAC  
GAGGACCTCTTCAAGTTCCTGGCTGACATGAGGCGCCCGTCGTCCCTGCTGCG  
GCGACTACGTCCTGTGACTGGTGCCTGGCACACCCCATACACAAGAAGTATC  
ACTC

Exon 84050 to 84270

GTGCAAACCGGTTCTTCCCTTCCCAGCCCAGCTCAAGATCGACATTTCTCCGG  
CTCCTGAAAATCCCCACTTCTGCCTCTCCCCTGAGCTGCTTCATATCAAGCCC  
TACCCGGACCCCAGGGGGCCGGCCACCAAGGAGATTCTGGAGTTCCCCGCCC  
GCGAAGTCTATGCCCCCATACCAGCTACAGGTACGGCCTCTGGGGCCCCAGC  
TGGGCACTTGA

Exon 87940 to 88130

GCCCCTGTCCCTCTGACACCCCCATCCTGCCCCCACAGGAACCTGCTGTACG  
TGTACCCGCACAGCCTCAACTTCAGCAGCCGCCAGGGCTCCGTGCGCAACCT  
TGCTGTGCGAGTGCGAGTACATGACAGGCGAGGACCCCAGCCAGGCTCTGCCG  
GTCAAGTGGCTGTGCCCCAGGGAAGGGGGGTAGGG

Exon 88140 to 88270

TGGGTCCCTCATGAATCCACTCTCCCAGGTCATCTTTGGCAAGTCCAGCTGCA  
GTGAATTTACCCGCGAGGCCTTCACACCGGTGGTCTACCATAACAAGTATGT  
AGGGGGACACGTGAGGAAGTGGGGG

Exon 88470 to 88680

GCCCCCAGCAGATCCCCCAGCCCGATTCTGCCAGGTCCCCCGAGTTCTACGA  
GGAGTTCAAGCTGCATCTTCCAGCCTGCGTGACAGAGAACCATCACCTGCTG  
TTACCTTCTACCATGTGAGCTGCCAGCCCCGGCCGGGCACTGCCCTGGAGAC  
ACCCGTGGGCTTTACTGTGAGCCGTCCCCTCCCTCCCTCCCCCTGAGCCCTCC  
T

Exon 88680 to 88870

TCGTCCCCCAACCTGGCCGCAGACCTGACCTCCAGCCTCTCCCCAGTGGATCC  
CACTGCTGCAGCACGGGCGCCTGAGGACCGGGCCCCTTCTGTCTCCCACTGTCT  
GTGGACCAGCCGCGCCGCCCAGCTATTCCGTGCTCACACCCGATGTATGTGCCCT  
GGAGCTCCTGCCTGCCAATGCACTGTCCCCAG

Exon 89360 to 89530

CAGGGAGGGCTGACCAGTGCCACCTGGTGCCTCCCTCCCACAGGTGGCGCT  
TCCGGGCATGCGCTGGGTGGACGGTCACAAGGGCGTGTTCAAGTGTGGAGCTC  
ACAGCCGTGTCTCTGTGCACCCCCAGGTACGGGGTGGGCGCGGAACCAAGA  
GTCCCGCCCTGCTCC

Exon 89660 to 89980

TTCATTCCCTGAGGCCCCACCCTGCTCACTCCACATCCCTACCCAGGACCCCT  
ACCTGGACAAATTCTTCACCCTGGTGCACGTCCTGGAGGAGGGAGCCTTCCC  
ATTCCGGCTCAAGGACACTGTGCTGAGCGAGGGCAACGTGGAGCAGGAGCTG  
CGGGCCAGTCTTGACGACTGCGCCTGGCCAGCCCCGAACCCCTTGTGGCCTT  
CTCCCACCACGTGCTGGACAAGCTCGTGCCTTGGTCATCAGGCCCCCGATC  
ATCAGTGGCCAGATTGGTAAGCGAATGTGGCCTCAGACCTCAGTTTCCCCATC  
CACATG

Exon 90480 to 90730

AGAGGCCTTGGGGCCCTGGAACCTTGACCTCTGCTCTGCCCTGCAGTGAACCTG  
GGCCGTGGAGCCTTTGAAGCAATGGCCCATGTAGTCAGCCTTGTTACCCGGA  
GCCTGGAGGCAGCCCAGGATGCCCGCGGTCACTGCCACAGCTGGCTGCCTA  
CGTCCACTACGCCTTTCGCCTTCTTGGCACTGAGCCCAGCCTCCCGGATGGTG  
AGTTTGTAGAAATCCCTGTGAGACGAGAAATATCTGGGAGAA

Exon 92870 to 93120

ATCACATCAGGTGGGTGGGTGGTTGACCCTATTCACTCCATCCTCAGGGGGCCC  
CTCCAGTGACAGTGCAGGCTGCCACACTGGCCCGTGGCTCTGGTCGCCCCGC  
AAGCCTCTACCTGGCGCGTTCCAAGAGCATCAGCAGCAGCAACCCTGACCTC  
GCCGTGGCCCCCTGGCTCTGTGGATGACGAGGTTTCCCGCATCCTGGCCAGCA  
AGGTAGGGCAACGGGGGGCCCTGGAATCTCCAGCCTCAGTGGT

Exon 97210 to 97390

GGCACCTCGCACTCTGTGACCCCTGCCTCTGTCCCCAGCTGCTTCACGAGGAG  
CTGGCTCTGCAGTGGGTGGTCAGCAGCAGTGCCGTACGCGAGGCCATCCTCC  
AGCACGCCTGGTTCTTCTTCCAGCTCATGGTGAGACCCCTCCTCCCTGCCTG  
GTGGCAAGAGACCCCCAGTGGAG

Exon 98770 to 98990

CAAATCCCACCCACAGCCCTCTACCCCCACCCCCAGGTGAAGAGTATGGCGC  
TGCACCTGCTGCTTGGCCAGCGACTAGACACACCCCGCAAGCTGCGCTTCCC  
CGGACGCTTCTTGGACGACATCACTGCCTTGGTGGGCTCTGTGGGCCTGGAG  
GTCATCACCCGTGTCCACAAGGTGAGAGATGCAGGGTCTCAATGTGGGAAGA  
AACCTGAGGGAGG



Exon 103130 to 103340

GGGGCTGAGGTTTGGGTGTGTGGGTGACAGGCACCTGTGTCCCCAGGATGT  
GGAGCTGGCCGAGCACCTCAACGCCAGCCTGGCTTTCTTCCTCAGTGACCTTC  
TGTCCCTGGTGGACCGGGGCTTTGTCTTCAGCCTGGTCCGGGGCCCACTACAAG  
CAGGTAGGAGTGGGCGTGGGCAGGGTGGGCATGGCATGGATGGAAGGCGGA  
GC

Exon 103340 to 103590

CAATGTTGACATCACTGATGGCCACCCCTCTCCTGCAGGTGGCCACGCGGCTC  
CAGTCGTCCCCCTAATCCAGCAGCCCTGCTGACCCTGCGCATGGAATTCACCCG  
CATCCTGTGCGAGCCACGAGCACTACGTGACCCTCAACCTCCCCCTGCTGCCCCC  
TGTCACCTCCAGCCTCGCCCTCCCCCTCTGTGTCCTCCACCACCTCCCAGGTG  
GGCTGCCTTCACTTCTGCCTCCTCTCTTTGACCTACAAC

Exon 103990 to 104220

TGACCCTTGACCGCTGGCATCCCCCATTTTTCCCCCACTCTGCAGAGCTCCAC  
CTTCTCCAGCCAAGCCCCGGACCCCAAGGTGACCAGCATGTTCTGAAGT  
GGACCATTCGGGAGCAGCACTTCCTAGCTGGGCTCCTGCTGACGGAGCTGG  
CACTGGCCCTCGAACCTGAGGCTGAAGGGTGAGCAGAGCTCCTGTCTAGCCC  
CAGGACAGGTGGGACAGTCCAG

Exon 104220 to 104480

GGAGCCATGTCCACCCTGTCCTGAGCACCTCATTACCCCATAGGGCATTCCCTG  
TTGCACAAGAAGGCCATCAGTGCTGTGCACAGCCTGCTATGTGGCCATGACA  
CTGACCCCCGCTACGCCGAGGCCACTGTGAAGGCTCGTGTGGCCGAGCTGTA  
CCTGCCACTGCTATCGATTGCACGGGATACCTTGCCACGGCTGCATGACTTTG  
CTGGTCAGTGGGCCAGGGGAAGATGGGGTCACATGATCCAGGGACTTGGTC

Exon 108850 to 109100

ACCAAGGGTTTATCTTTCTTTCCCTCTGTCTTTCCCTGCCAGAGGGCCCAGGTC  
AGCGGTCAAGACTGGCCTCAATGCTTGACTCAGACACAGAAGGCGAAGGGG  
ACATTGCGGGTACCATCAACCCCTCTGTGGCCATGGCCATTGCTGGTGGCCCC  
CTAGCCCCTGGCTCCCGGGCCAGCATCTCCAGGGGCCACCAACGGTGAGTA  
GGGAGGCTTGTCCCCATAGACATCATCCACTTTGAATGAGA

Exon 109140 to 109410

TCACATGGAGAAAATGGAAATTGACTTTGATTCTCTCTGGCCCCAGGCTTCT  
CGCGCAGGCTGTGCCCTCTCTGCTGAGTCAAGCCGGACCTTGCTGGCGTGTGT  
GCTGTGGGTGCTGAAAAACACCGAGCCGGCGCTCCTGCAGCGCTGGGCCACT  
GACCTGACACTCCCCCAGCTGGGACGTCTGTTGGATTTGCTGTACCTTTGCCT  
AGCTGCCTTTGAGTACAAGGTTTGAGGGCGTGCGCAGGAGATGATGGAGGAG  
GCAGGCTA

Exon 110310 to 110530

GAAAAGAGCAGAGTCAGCCTGGAACCCCAAGTTCTCTGCACCCCCAGGGGAA  
AAAGGCCTTTGAACGCATCAACAGCCTCACATTCAAAAAATCTCTGGATATG  
AAGGCGCGGCTAGAGGAAGCCATTCTGGGTACCATCGGAGCTCGACAAGAA  
ATGGTTCGGCGAAGTCGTGGTAAGAGGGTGACATACCCACGTGTCCCCATCC  
CACCAGCTGCTCCCA

Exon 110770 to 110940

TGTGTTTTTACGCATCTGTGATCGTGCACCCACGCGTCTCAGAGAGGAGCCCG  
TTTGGGAATCCGGAGAATGTGCGCTGGCGGAAGAGCGTCACACACTGGAAGC  
AAACCTCAGACCGCGTGGACAAGTAGGTGTGGGCAGGAGGGTGTCTGCTGAG  
TTCAGAACAGTTTG

Exon 111590 to 111770

ATCTCACCCCGAGTGGGCCCCCAAGACCTCCTTTCCCCTTCCAGGACCAAGG  
ATGAAATGGAACACGAGGCCTTGGTGGAAGGGAACCTGGCAACCGAGGCAA  
GCCTAGTGGTTCTGGACACACTGGAGATCATCGTGCAGGTAGGGCTTGATCC  
AGCATCTGCCTTGTGCTCTGAGCCCA

Exon 111830 to 112050

ACCCTAGGCTCTAACACCTGGATTTCTGACCCCCTTCCCTCCAGACGGTGATG  
CTTTCAGAAGCCCCGGGAGAGCGTCTTGGGGGCAGTGCTGAAGGTTGTGCTGT  
ACAGCCTGGGCAGTGCCCAGAGTGCCCTCTTCTTGACAGCATGGCCTGGCCAC  
CCAGAGGGCCCTTGTGTCCAAGGTGAGCACCCTCAACAACCATGATTCTTA  
GAAAAACAGTAG

Exon 112910 to 113140

AACGGGGAGGGGCTGGACAGTGTCTGTCTGGGTCTTGGGGGCAGTTCCCGG  
AGCTGCTGTTTCGAGGAGGACACGGAGCTGTGTGCCGACCTGTGCCTGAGGCT  
CCTACGACACTGTGGCAGCCGCATCAGCACCATCCGCACGCACGCCAGCGCC  
TCGCTGTACCTGCTCATGCGACAGAACTTCGAGATCGGCCACGTGAGTGGGG  
GCTAGGAGGCATGGTCCACACATGGCTCTGGTC

Exon 114090 to 114340

TCTGAGACTCCCGGCTCCACCCTCCCGCCCCCTGTCCCTGCAGAACTTTGCCCG  
TGTGAAGATGCAGGTCACCATGTCTCTCTCGTCCCTGGTGGGGACGACGCAG  
AACTTCAGTGAAGAGCACCTGCGACGTTCACTCAAAACCATCCTCACCTATG  
CTGAGGAGGACATGGGGCTGCGGGACAGCACCTTCGCAGAGCAGGTGACAC  
CTGCTGGGTCCCCGCCCCGCCTCCCCTTCATATAACTCCCAAC

Exon 114370 to 114550

ATGCTCTCATTGGCCCCCTGGACGTTCCCCGGCTCCAGGTCCAGGACCTGATGT  
TCAACCTGCACATGATCCTGACGGACACGGTGAAGATGAAGGAACACCAGG  
AGGACCCTGAGATGCTCATCGACCTCATGTACAGGTGAGGTGGGCCAGCTGG  
CACCTTCAGCCACGCCCACGCCCA

Exon 116900 to 117170

AGGTGAGTCCCCTCCTCACATCCCCCCTCACCTGGACTCCAGAATTGCCCGGG  
GCTACCAGGGCTCACCGGACCTTCGGCTGACCTGGTTGCAGAACATGGCCGG  
GAAGCACGCGGACGTGGGCAACCACGCCGAGGCCGCCAGTGCA  
CGCGGCCGCCCTCGTGGCTGAGTACCTCGCCCTGCTCGAGGACCAGCGCCAC  
CTGCCCCGTGGCTGGCGATTTCTTCCAGGTGAGTGGCCAGGGGTTGGCAGGT  
GGCGGACGGCA

Exon 117170 to 117410

ACGAGTGCAGTGGGGACCAGGGTCTGACGCCACCTCTCCACCCCAGAACAT  
CTCATCCAACGTGCTAGAGGAGTCCGCCATCTCCGACGACATCCTGTCGCCC  
GACGAGGAGGGCTTCTGCTCCGGGAAGCACTTCACTGAGCTGGGGCTGGTAG  
GGTTGCTGGAACAGGCAGCCGGCTACTTCACCATGGTGAGGCCTTGGGGACT  
GGGTGCAGGAGAGGGGGCTCGGGCCAGGGAGGT

Exon 121670 to 121900

GAGAGGAAGACAGTTTGGGGAATCCTGACCCACCTCACCTCAGGGCGGGC  
TCTACGAGGCGGTGAATGAGGTCTACAAGAACCTCATCCCCATCCTGGAAGC  
CCACCGTGACTACAAGAAGCTGGCCGCGGTGCACGGCAAACCTGCAGGAGGC  
CTTCACCAAGATCATGCACCAGGTGGGCCAGGACCCCTCCCCAGACCCA  
CCCTCAGCCCCACTCCTCATCC

Exon 121910 to 122000

CCCCAGGGATCTGCTGACCTTGACCCTTCTCTTCCCCACAGAGTTCGGCTGG  
GAGGTGAGTCAGCCTTGGTGGACAGCCACCTGCCTCTG

Exon 123290 to 123510

TCCAGCAGGGGCCTCCCGGACAACCACACCCTTTCTCACAGCCCCAGCGCGT  
GTTTCGGGACGTATTTCCGCGTGGGCTTCTACGGCGCCCACTTCGGTGACCTGG  
ATGAGCAGGAGTTTGTGTACAAGGAGCCATCGATCACGAAGCTGGCAGAGAT  
CTCACACCGGCTGGAGGCATGTCCTTGTGGTTGGGGGTGGAACGGGGCATGG  
GGCTGCCTTGGG

Exon 123510 to 123633 (end clone)

GGCTGGAGTAGGGGCTGTCCCTGGGTGGCCCCGAGTCAGCCCTGTGTCTCCA  
GGAGTTCTACACGGAGAGATTTGGCGACGACGTCGTTGAGATTATCAAAGAC  
TCTAACCTGTGGACAAGTC

Human CLASP-7 promoter region , 61938 (beginning of contig) to 63888 (end of first predicted exon)

GGGCATGTGGCTCATTCTGTAAATCCCGGCACTTTGGGAGGCCGAGGCGGGTGGATC  
ACCTGAGGTCAGGAGCTCCAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTAC  
TAAAAATACAAAAAATTAGCCAGGTGTGATGGTGGGTGCCTGTAATCCCAGCTACTC  
GGGAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGCAGAGGTTGCGGTGAGCC  
GAGATTGTGCCATTGCACTCCAGTCTGGGCAACAAGAGCGAAATGCCACCTCAAAT  
AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAGAGGATAA  
AATGCCAGCAACCCATAGATGGGAATGAGAACAGCACGTGCAAAGGCCCTGAGGCA  
GAGCCACGGCCTTGTCTGATTCAACCTCAAATTCTCCCTGGGGCATTGTCTGACCAGG  
GAAAGAAGGGCTGTCCAGGAGGAAGGACCTGCCGGTGCAGAGGCATGCAGGTGAGA  
AAGGGGTGAGCTCCTCCAGAGGGGAGTGTGCGCTGGAGAATTCTCTAAAAATGCTGC  
AGCAGTGCTGGGAGAGAGGCCAGTGGGGAGAGATTTGAGACCATAGATTAACCAAG  
ACATCCCCACCTCTTCTCTTGGTAGAGGCGGCCCGAAAGTCTAGACTCCCAAAT  
GGCTCACTCAGGTCCCACCACCTGGACCTGGGGCACATCTCCGAGCACTCCAGTGCC  
TAGCCAGGCTCCTCTGACTCCCATGCTGTAGACTGGGAGCACGGACAATGCAGGCGC  
TGGAGACCCCTGTGAGTCACACTGAGCAAGCACCCGAACACCTCTGTGCCTCAGTTT  
ACTCATCTGTAAAAGGAGGAAAACAATAATTTCTTCTGCATGTGTGAATTGCAGGGC  
CAGGCTCAATGACATCTTAGCAATTAGACTTTTTGAGACAGGGTCTCGCTCTGTCAAC  
CAGGCTGGATTGAAATGGCACAATCACAGCTCACTGCAGCCTTGACCTCCCAGGCTC  
AAGCGATCCTCCTCCCTCAGACTCCCAAGTAGCTGAGATTACAGGCACACACCACCA  
TGCCTGGTTAATTTTTGCAATTTTTGTGGACACGGGGTCTCATTATGTTGCCAGGCT  
GGTCTCCAACCTCCTGGGCTCAAACAATCCTCCTGCCTTGGCCCCCACAGTGCTGGG  
ATTACAGGCATGAGCCACCATGCACGGCCACGATTATACTTACAGGTATGATTATTA  
GATACATGAACATCGTTATTGTTTTCCAGCCAGGAGTCAGAGGGCAGAAAGAGCGCC  
CCCCAAACCCCGGAAATCTGGGGCCTACCCAGCCTGGGTCCAGCGCCTCCCCTCCC  
TCCCTCCCTCCTGAGCTTCAGTTTCCCCAGCCCTGCTCCTGGGGTGGTAAGACCACCC  
CACTAAACCCCGGGAGCCTGGGGTCCACCTAGCCCGGGTCTCAGCGCCTCCCTTCCC  
TCCCTCCCTCCTCAGGCTCAGTTTCTCCAGCCCAGCTCCAGGGTGGAAAGAGCGCC  
CCCGCCAGCTCGGGAGTCTGGGGCACCCCCAGTCTGGGTCCAGCGCCTCCTCTCCC  
TAACTTCCCTCCTCAGCCTCAGTTTCCCCAGCCCTTCTCCTAGGGTAGAAAGAGCGTC  
CCCCCAGCCCGGGAGTCTGGGGCCCCGCCAGCCTGGATCCCGGGGCCTCCTCTCCGT  
CCCCAGCCTCAGTTTCCCCAGCCCCAGGACTCCAGGCGACCCCTCCGGCCTGCAGG  
GGCAGCACGGAGCGGCCCGGGCCACCCGGAAGGGCCCCCGCCCCGCGCCGGCCCCG  
CCCCGCCCCGGCTGCCAGAACCGGGAGGCGGCGGCGGCGGGGCCGGGGCCCCG  
GGGCGGCGGCGGCGGGACGCGAGGACCATGGCTGCCTCCGAGCGCCGCGCCTTCGC  
GCACAAGATCAACAGG

FIG. 6

hCLASP4	-----MFPMEDISISVIGRQRTVQ-----	20
hCLASP5	-----MTHLNSLDVQLAQELG-----	16
hCLASP3	-----MAERRAFAQKISRTVAAEVKQISGQYSGSPQLLNINIVG	41
hCLASP2	-----MLLFPYDDFQTAILRRQGRYICS-----	23
hCLASP7	-----MAASERRAFAHKINRTVAAEVKQVSRERSGSPHSSRRCSSSL	43
hCLASP1	MSFRGKVKREPSEFWKKRRTVRRVIOEEFHRFSSQEKPRLLEPLDYETVIEELEKTYRN	60
...		
hCLASP4	-----STVPEDAEKRAQSLFVKECIKTYSTDWHVVNYK	53
hCLASP5	-----DFT	19
hCLASP3	N-----ISHHTTVPLTEAVDPVDLEDYLITHPLAVDSGPLRDLIEFP	83
hCLASP2	-----TVPKAEQSLFVTECIKTYNSDWHLVNYK	55
hCLASP7	G-----VPLTEVVEPLDFEDVLLSRPPDAEPGPLRDLVEFP	79
hCLASP1	DPLQDLLFFPSDDFSAATVSWDIRTLYSTVPEDAEHKAENLLVKEACKFYSSQWHVVNYK	120
::		
hCLASP4	YEDFSGDFRMLPCKSLRPEKIPNHVFEIDEDCEKDED-----SSSLCSQKGGVIKQG	105
hCLASP5	DDDLDVVFTPKCRTLQP-SLPEEGVELDPHVR-----DCVQTYIREWLI	63
hCLASP3	PDDIEVVYSPRDCRTLVS-AVPEE-SEMDPHVR-----DCIRSYTEDWAI	126
hCLASP2	YEDYSGEFRQLPNKVVKLDKLPVHVYEVDEEDVDKDED-----AASLGSQKGGITKHG	107
hCLASP7	ADDLELLQPRECRTEP-GIPKD-EKLDQVR-----AAVEMYIEDWVI	122
hCLASP1	YEQYSGDIRQLPRAEYKPEKLPSHSFEIDHEDADKDEDTTSHSSSKGGGGAGGTGVFKSG	180
:: .                    * .    :: .		
hCLASP4	WLHKANVNSTIT--VTMKVFKRRYFYLTQLPDGSYILNSYKDEKNSKESK-GCIYLDACI	162
hCLASP5	VNRKNQGSPEIC--GFKKTGSRKDFHKT-LPKQTFESETLECSEPAAQA--GPRHLNVLC	118
hCLASP3	VIRKYHKLGTGF--NPNTLDKQKERQKG-LPKQVFESDEAPDGSYQDDQDDLKRRSMSI	183
hCLASP2	WLYKGNMNSAIS--VTMRSFKRRFFHLIQLGDGSYNLNFYKDEKISKEPK-GSIFLDSCM	164
hCLASP7	VHRRYQYLSAAY--SPVTTDTQRERQKG-LPRQVFEQDASGDERSGPEDSNDSTRGSGSP	179
hCLASP1	WLYKGNFNSTVNNTVTVRSFKKRYFQLTQLPDNSYIMNFYKDEKISKEPK-GCIFLDSC	239
: :                    . . .                    *                    : :                    . . .		
hCLASP4	DVVQCPKMRRHAFELKMLDKYSHYLAETEQUEMEEWLITLKKIIQINTDSLQVEKKETVE	222
hCLASP5	DVSGKGVPVTACDFDLRLSLQDPKRLNLLQQVSAEDFEKQNEEARRTN-----RQAE	169
hCLASP3	DDTPRGSWACSI FDLKNSLPDALLPNLLDRTPNEEIDRONDDQKSN-----RHKE	234
hCLASP2	GVVQNNKVRRAFELKMQDKSSYLLAADSEVEMEEWITILNKILQLN-----FEAAMQEK	219
hCLASP7	EDTPRSSGASSIFDLRLNLAADSLPSLLERAAPEDVDRRNETLRRQH-----RPPA	230
hCLASP1	GVVQNNRLRKYAFELKMNDLTYFVLAAETESDMDEWIHTLNRILQISPEGPLQGRSTEL	299
* : :                    .                    : :                    .                    :		
hCLASP4	TAQDDTSS-----QGKAENIMASLERSMHPMLKYGRETEQLNKL SRGDGRQNLFSFDSE	278
hCLASP5	LFALYPSVD-----EEDAVEIRPVPECPEHLG-----N-----RILVKLLTLKFEIE	212
hCLASP3	LFALHPSPD-----EEPIERLSVPDIPKEHFG-----QRLLVKCLSLKFEIE	277
hCLASP2	RNGDSHEDD-----EQSKLEGSGGLDSYLP ELAKSAREAEIK---LKSESrvkLFYLDPD	272
hCLASP7	LLTLYPAPD-----EDEAVERCSRPEPPREHFG-----QRLVKCLSLKFEIE	273
hCLASP1	TDLGLDSLNSVTCECTPEETDSSNNLHADFAKYLTETEDTVKTTNRMERLNLFSLDPD	359
:                    :                    :                    :                    : : : :		
hCLASP4	VQRLDFS-----GIEPDIKP-FEEKCNKRLVNCHDLTFNILGQIGDNAKGPPTNVEPFFI	333
hCLASP5	IEPLFAS-----IALYDVKERKKISENFHCDLNSDQFKGFLRAHTPSVAASSQARSVFSV	268
hCLASP3	IEPIFAS-----LALYDVKEKKKISENFYFDLNSEQMKGLLRPHVPPAAITTLARSAIFSI	333
hCLASP2	AQKLDFS-----SAEPEVKS-FEEKFGKRI LVKCNLDSFNLQCCVAENEEGPTTNVEPFFV	327
hCLASP7	IEPIFGI-----LALYDVREKKKISENFYFDLNSDSMKGLLRAGTHPAISTLARSAIFSV	329
hCLASP1	IDTLKLQKDLLEPESVIKPFEEKA AKRIMIICKALNSNLQGCVTENENDPITNIEPFFV	419
: :                    . :                    : . . .                    :                    . : .                    * : :		

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hCLASP4	FKSHLESTIYTQDLHVHKFFHHCQLIQS-----GSKEVPGELIKYLKCLHAM	794
hCLASP5	IEVAVSSVHTQDNHLEKFFTLCHSLESQVTFPIRVLDQKISEMALEHELKLSIICLNSS	715
hCLASP3	VEVAVSSIHTQDPYLDKFFALVNALDEH-LFPVRIGDMRIMENNLLENELKSSISALNSS	780
hCLASP2	ISTHLVSTVYTQDQHLNFFQYQCKTES-----GAQALGNELVKYLSLHAM	787
hCLASP7	VELTAVSSVHPQDPYLDKFFTLVHVLEEG-AFPFRLKDTVLEGNVEQELRASLAALRLA	767
hCLASP1	VSTFVSTVNTQDPHVNAFFQECQKREKD-----MSQSPTS NFIRSKNLLNVE	887
	.. : : . * : : * : : *	
hCLASP4	EIQVMIQFLPVILMQLFR-----VLTNMTH-----EDDVP	824
hCLASP5	RLEFLVLFLHLVLDKLEQLSVQPMVIAGQTANFSQFAFESVVAIANSLHNSKDLSKDQHG	775
hCLASP3	QLEFVVRFLHLLLDKLIILLVIRPPVIAGQIVNLGQASFEAMASIINRLHKNLEGNHQHG	840
hCLASP2	EGHMI AFLPTILNQLFR-----VLT-RAT-----QEEVA	816
hCLASP7	SPEPLVAFSHHVLDKLVRLVIRPPIISGQIVNLGRGA FEAMAHVVS LVHRSLEAAQDARG	827
hCLASP1	KIHAIMSFLPIILNQLFK-----VLVQNE-----EDEIT	916
	. : : * : : *	
hCLASP4	INCTMV-LLHIVSKCHEEGLDS-----YLRSEFIKYS-----FRPEKP	860
hCLASP5	RNCLLASVYHYVFRLEPVQRDVPKSGAPTALLDPRS YHTYGR TSAAAVSSKLLQARVMSS	835
hCLASP3	RNSLLASYIHYVFRLEPNTYPNSSSPG-PGGLGGSVHYATMARSAVRPASLNLNRSRSLN	899
hCLASP2	VNVTRV-I IHVVAQCHEEGLES-----HLRSYVKYA-----YKAEPY	852
hCLASP7	HCPQLAAYVHYAFRLPGTEPSLPDGAPP-----VTVQAATLARGSGRPASLYLARSKSISS	883
hCLASP1	TTVTRV-LPDI VAKCHEEQLDH-----SVQSYIKFV-----FKTRAC	952
	. . . :	
hCLASP4	SAPQAQLIH-----ETLATTMIAILKQS-----	883
hCLASP5	SNPDLAGTHSAAD EEVKNIMSSKIADRNCSRMSYYCSGSSDAPSSPA-----	882
hCLASP3	SNFDISGTPSPDDEVSRIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAESTQAMDRSC	959
hCLASP2	VASEYKTVH-----EELTKSMTTILKPS-----	875
hCLASP7	SNPD LAVAPGSVDDEVSRI LASKLLHEELA-LQ-----	915
hCLASP1	KE---RPVH-----EDLAKNVTGLLKS N-----	972
	: . .	
hCLASP4	-----ADFLSINKLLKYS-----WFFFEIIAKSM	907
hCLASP5	-----APRPASKKHFEELALQ-----MVVSTGMVKSM	910
hCLASP3	NRMSSHTETSSFLQTLTGRLP TKLFHEELALQWVVC SGSVRESALQQAWFFFEIMVKSM	1019
hCLASP2	-----ADFLTSNKLLRYS-----WFFFDVLIKSM	899
hCLASP7	-----WVSSSAVREAILQHA-----WFFFQLMVKSM	942
hCLASP1	-----DSPTVKHVLKHS-----WFFFAILKSM	995
	. * . . : ***	
Cadherin Cleavage		
hCLASP4	ATYLLEENKIKLERGQREFPETYHHVLHSLLLAIIPHVTIRYAEIPDE---SRNVNYSLAS	964
hCLASP5	AQHVHNMMDKRDSERRTRESDRFMDDITTIVNVVTSEIAALLVKPQKENEQA EKMNISLAF	970
hCLASP3	VHHL YFNDKLEAEKRSRPERFMDDIAALVSTIASDIVSRFQKDTM---VERLNTSLAF	1076
hCLASP2	AQH LIENSKVKLI RNQREFPASYHHAETVVMMLMPHITQKFGDNPEA---SKNANHSLAV	956
hCLASP7	ALHLLLGQRLDTERKLRFPGRFLDDITALVGSVGLVITRVHKDVEL---AEHLN ASLAF	999
hCLASP1	AQHLIDTNKIQLHRPQRFPE SYQNELDNLMVLS DHVIWKYKDALEE---TRRATHSVAR	1052
	. : : . : * * . : . : : . . . * : *	
hCLASP4	FLKRCLTLMDRGFIENLINDYISGFSPKDP----KVLA EYKFEFLQ TICNHEHYIPLNL	1019
hCLASP5	FLYDLSLMDRGFVENLIRHYCSQLSAKLSNL---HTLISMRL EFLRILCSHEHYLNLNL	1027
hCLASP3	FLNDLLSVMDRGFVESLIKSCYKQVSSKLYSLPNPSVLVSLRLDFLR IICSHEHYVTNLNL	1136
hCLASP2	FIKRCFTFMDRGFVEKQINNYISCFAPGDP----KTLFEYKFEFLRVVCNHEHYIPLNL	1011
hCLASP7	FLSDLLSLVDRGFVESLVRAHYKQVATRLQSSPNPAALLTLRMEFTRILCSHEHYVTNLNL	1059
hCLASP1	FLKRCFTFMDRGCFVEMVNNYISMFS S GDL----KTLCOYKFDFLQEVQCHEHFIPCLL	1107
	* : : : * * : * . : : * : : * : * : *	

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Cadherin EC motif

hCLASP4 PMAFAKPKLQR-----VQDS--NLEYSLSDEYCKHHFLVGIILLRETSI 1060  
hCLASP5 FFMNADTAPTSP--CPSISSQSSSSCSFQDQKIASMFDLTSEYRQOHFLTGLFTTELAA 1085  
hCLASP3 PCSLLTPPASPSPSVSATSQSSGFSTNVQDQKIANMFELSVPFROQHLAGIVLTELAV 1196  
hCLASP2 PMPFGKGRIQR-----YQDL--QLDYSLTDEFCRNHFLVGIILLREVGT 1052  
hCLASP7 PCCPLSPASPSPSVSSTTSQSSTFSSQAPDPKVTSMFELSGPFRQOHFLAGIILLTELAL 1119  
hCLASP1 PIRSANIPDPLTP-----SES-----TQELHASDMPEYSVTNEFCRKHFLIGILLREVGF 1157  
. . . . . : : : : : \* \* \* \* \* : : .

hCLASP4 ALQDN----YEIRYTAISVIKNLLIKHAFDTRYQHKNQOAKIAQLYLPFVGLLLENIORL 1116  
hCLASP5 ALDAEGEGISKVQRKAVSAIHSLLSSHDLDPKVCPEVKVKIAALYLPVGIILLDALP-- 1143  
hCLASP3 ILDPDAEGLFGLHKKVINMVHLLSSHSDSPRYSDPOIKARVAMLYLPLIGIIMETVP-- 1254  
hCLASP2 ALQEFR----EVRLIAISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVORI 1108  
hCLASP7 ALEPEAEGAFILHKKAISAVHSLLCGHDTDPYAEATVKARVAELYLPLLSIARDTLP-- 1177  
hCLASP1 ALQEDQ----DVRHLALAVLKNLMAKHSFDDRYREPRKQOQIASLYMPPLYGMLLDNMPRI 1213  
\* : : : : \* \* \* : : \* \* \* : : : :

hCLASP4 AGRDTLYSCA-----AMPN-S---ASRDEFP CGFTSPANRGSLSSTDKDTAYGS 1160  
hCLASP5 -----QL-----CDFTVADTRRYRTSGSD----- 1162  
hCLASP3 -----QLY-----DFTETHNQGRPICIAATDD-- 1276  
hCLASP2 NVRDVSPFPVNAGMTVKDESALPA-VNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTT 1167  
hCLASP7 -----RLH-----DFAEGPGQRSRLASMLDSDTE 1201  
hCLASP1 YLKDLYPFTVNTSNQGSRDDLSNNGGFQSQTAIKHANSVDTSFSKDVLSIAAFSSIAIS 1273  
. . . . .

hCLASP4 FQ-NGHGIKREDSRGS LIPEGATGFDPQGN TGEN-----TRQSSTRSSVSQYNRLDQYE 1213  
hCLASP5 -----EEQEGAGAINQNALAIAGNNFNLT-----SGIVLSSLPYKQYNMLNADT 1208  
hCLASP3 -----YESESGSMISQTVAMAIAGTSVPQLTR-----PGSFLTSTSGRQHTTFAES 1324  
hCLASP2 STPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSE 1227  
hCLASP7 -----GEGDIAGTINPSVAMAIAGGPLAPGSR-----ASISQGPPTASRAGCALSAS 1249  
hCLASP1 -----TVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPLALIGSTLRFDRLDQAE 1327  
. : : : . . . . .

hCLASP4 IRSLLMCYLYIVKMISEDTLLTYWNKVSPOELINILILLEVCLFHFRYM GKRN IARVHDA 1273  
hCLASP5 TRNLMICFLWIMKNADQSLIRKWIADLPSTQLNRILDLLFICVLCFEYK GKQSSDKVSTQ 1268  
hCLASP3 SRSLICLLWVLKNADETVLQKWFTDLSVLQNLRLDLLYLVCVSCFEYK GKKVFERMNSL 1384  
hCLASP2 IKSLLMCFLYILKSMSDDALFTYWNKASTSELM DFFTISEVCLHQFYMGKRYIARNQEG 1287  
hCLASP7 SRTLLACVLWVLKNTEPALLQRWATDLTLPQLGRLLDLLYLCLAAFEYK GKKA FERINSL 1309  
hCLASP1 TRSLLMCFLHIMKTISYETLIAYWQRAPSPESVDFFSILDVCLQNFYRLGKRN IIRKIAA 1387  
: : \* \* : \* : : : : : : : : \* \* \* : :

hCLASP4 WLSKHFGIDR-----KSQTMPALRNRSGVMQARLQHLSSLESS----- 1311  
hCLASP5 VLQKSRDVKAR-----LEEALLRGE GARGEMRRRAPGNDRFPGLNEN--- 1311  
hCLASP3 TFKKSKDMRAK-----LEEAILGSIGARQEMVRRSRGQLERSPSGSAFGSQ 1430  
hCLASP2 LGPIVHDRKS-----QTLFVSRNRTGMMHARLQQLGSLDNS----- 1323  
hCLASP7 TFKKS LDMKAR-----LEEAILGTIGARQEMVRRSRERSPFGNPEN---- 1350  
hCLASP1 AFKFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHKQHR SQTLP IIRGKN---- 1442  
. . . . .

hCLASP4 -----FTLNHSSTTTEADIFHQALLEGNTATEVSLTVLDTISFETQCFKTQLL 1359  
hCLASP5 --LRWKKEQTHWRQANEKLDKTKAE L DQEALISGNLATEAHLIILDMQENITQASS-ALD 1368  
hCLASP3 ENLRWRKDMTHWRQNT EKLDKSR AEIEHEALIDGNLATEANLIILDTLEIVVQTVS-VTE 1489  
hCLASP2 -----LTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLEFLAFKNQLL 1371  
hCLASP7 --VRWRKSVTHWKQTS DRVDKTKIEMEHEALVEGNLATEASLVVLDTLEIIVQTVM-LSE 1407  
hCLASP1 --ALSNPKLLQMLDNTMTS NSNEI DIVHHVDTEANIATEGCLTILDVLSLETQTHQRQLQ 1500  
. . . : : : . \* \* \* \* \* . . .

FIG. 7  
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hCLASP4 NNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFISKFPFAFFKGRVNMCAAFY 1419  
hCLASP5 CKDS---LLGGVLRVLVNSLNCDSSTTYLTHCFATLRALIAKFGDLLFEEVEQCFDLCH 1425  
hCLASP3 SKES---ILGGVLKVLHSMACNQSAVYLQHCFFATQRALVSKFPELLFEEETEQCADLCL 1546  
hCLASP2 ADHGHNPMLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRADMCAALCY 1431  
hCLASP7 ARES---VLGAVLKVVLYSLGSAQSALFLQHGLATQRALVSKFPELLFEEDTELCADLCL 1464  
hCLASP1 QCDCQNSLMKRGFDTYMLFFQVNSATALKHVFASLRLFVCKFPFAFFQGPADLCGSFCY 1560  
. : : : : \* \* : : : \* : : \* : : \* : \*

hCLASP4 EVLKCCTSKISSTRNEASALLYLLMRNFEYTKRKTFLRTHLQIIIVASQLIADVALSGG 1479  
hCLASP5 QVLHHCSSSMDVTRSQCATLYLLMR--FSFGATSNFARVKMQVTMSLASLVGRAPDFNE 1483  
hCLASP3 RLLRHCSSTIGTIRSHPSASLYLLMR--QNFEIGNNFARVKMQVPMSSSLVGTSONFNE 1604  
hCLASP2 EILKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTHLQVIIISVSQLIADVVGIGE 1491  
hCLASP7 RLLRHCGSRISTIRTHASASLYLLMR--QNFEIGHNFARVKMQVTMSLSSLVGTTONFSE 1522  
hCLASP1 EVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSHLQLIKAVSGLIADAG-IGG 1619  
.: : \* : : : \* : : : \* : : : : : \*

hCLASP4 SRFQESLFIINNANSRPMKATAFPAEVKDLTKRIRTVLMATAQMKHEKDPPEMLIDLQ 1539  
hCLASP5 EHLRRSLRTILAYSEEDTAMQMTFFPTQVEELLCLNLSILYDTVKMREFQEDPEMLMDLM 1543  
hCLASP3 EFLRRSLKTILTYAEDLELRETTFPDQVQDLVFNLMILSDTVKMKHEQEDPEMLIDLQ 1664  
hCLASP2 TRFQQSLSIINNANSRDLIKHTSFSSDVKDLTKRIRTVLMATAQMKHEHNDPEMLVDLQ 1551  
hCLASP7 EHLRRSLKTILTYAEDMGLRDSTFAEQVQDLVFNLMILSDTVKMKHEQEDPEMLIDLQ 1582  
hCLASP1 SRFQHS LAITNNFANGDKQMKNSNFPFAEVKDLTKRIRTVLMATAQMKHEKDPPEMLVDLQ 1679  
: : : \* : : : \* : : : \* : : : : : \*

transmembrane

hCLASP4 YSLAKSYASTPELRKTWLDSDMAKIHVKNGDFSEAMCYVHVAALVAEFLHRKK----- 1592  
hCLASP5 YRIAKSYQASPDRLRLTWLQNMAGKHTKKKQYTEAMCLVHAAALVAEYISMLEDH----- 1598  
hCLASP3 YRIAKGYQTSPE-RLTWLQNMAGKHSERSNHAEEAQCCLVHSAALVAEYISMLEDR----- 1718  
hCLASP2 YSLAKSYASTPELRKTWLDSDMARIHVKNGDLSEAMCYVHVTALVAEYITRKG----- 1604  
hCLASP7 YRIARGYQGPSDLRLRLTWLQNMAGKHAELGNHAEAAQCMVHAAALVAEYIALLEDQ----- 1637  
hCLASP1 YSLANSYASTPELRRTWLESMAKIHARNGDLSEAMCYIHIAALIAEYIKRKG YWKVEKI 1739  
\* : : \* : : \* : : : \* : : : : : \*

hCLASP4 -----LFPNGCSAFKKITPNIDEEGAMKEDAGMMD----- 1622  
hCLASP5 -----SYLPVGSVSFQNISSNVLEESVVSSEDTLSPDEGTV 1633  
hCLASP3 -----KYLPGVCVTFQNISSNVLEESAVSDDVVSPEDEGI 1753  
hCLASP2 -----VFRQGCTAFRVITPNIDEEASMMEDVGMQD----- 1634  
hCLASP7 -----RHLPVGCVSFQNISSNVLEESAISDDILSPDEEGF 1672  
hCLASP1 CTASLLSEDTHPCDNSNLLTTPSGGSMFSMGWPAFLSITPNIKEEGAAKEDSGMHD----- 1795  
: \* : \* : : : \* : : \*

ITAM

hCLASP4 ---VHYSEEVLLELLEQCVDGLWKAERYEIISEISKLVPIYIEKRREFEKLTVYRTIHG 1679  
hCLASP5 CAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKLVIPILEAHREFRKLTLTHSKLQR 1693  
hCLASP3 CSGKYFTESGLVGLLEQAAASFMSAGMYEAVNEVYKLVIPILEANRDAKKLSTIHGKIQE 1813  
hCLASP2 ---VHFNEVDLMELLEQCADGLWKAERYELIADIYKLIPIYIEKRR----- 1677  
hCLASP7 CSGKHFTELGLVGLLEQAAGYFTMGGLYEAVNEVYKNLIPILEAHRDYKKLAHVHGKIQE 1732  
hCLASP1 ---TPYNENILVEQLYMCGEFLWKSEYELIADVKNKPIIAVFEKQDFKKLSDIYYDIHR 1852  
: \* : \* : : : \* : : \*

ITAM DOCK motif DOCK motif ITAM

hCLASP4 AYTKILEVMHTKKRLLGTFFRVAFYQGSEFFEEEDGKEYIYKEHKLTLGLSEISRLVLYG 1739  
hCLASP5 AFDSIVNKDH--KRMFGTYFRVGEFG-SKFGDLDEQEFVYKEHAITKLPEISHRLEAFY 1750  
hCLASP3 AFSKIYHQSTGWERMFGTYFRVGEFG-TKFGDLDEQEFVYKEHAITKLAEISHRLEAFY 1872  
hCLASP2 -----DFFEDDGKEYIYKEHKLTLPLSEISORLLKIYS 1710  
hCLASP7 AFTKIMHQSSGWERVFGTYFRVGEFG-AHFGDLDEQEFVYKEHSITKLAEISHRLEEFY 1791  
hCLASP1 SYLKVAEVVNSEKRLFGRYRVAFYQGSEFFEEEDGKEYIYKEHKLTLGLSEISORLLKIYA 1912  
: : : : : \* : : : \* : : : : \*

FIG. 7  
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	ITAM	ITAM	
hCLASP4	EKEFGTENVKIIQSDSKVNAKELDPK	YAHYIQV	TYVVKHYFDDKELTERKTEFERNHNISRFV 1799
hCLASP5	QCFGAEFVEVIKDSPTVDKTKLDPN	KAYIQI	TFVEHYFDEYEMKDRVITYFEKNFNLRFRM 1810
hCLASP3	ERFEGEDVVEVIKDSNPVDKCKLDPN	KAYIQI	TYVEHYFDTYEMKDRITYFDKNYNLRFRM 1932
hCLASP2	DKFGESENVKMIQDSGKVNPKDLDSK	YAYIQV	THVHFFDEKELQERKTEFERSHNIRFRM 1770
hCLASP7	ERFGDDVVEIIKDSYPVDKSKLDSK	KAYIQI	TYVEHYFDTYELKDRVITYFDRNYGLRTFL 1851
hCLASP1	DKFGADNVKIIQDSNKNVPKDLDPHY	YAYIQV	TYVTFEFEEKEIEDRKTD FEMHHNINRFV 1972
	: ** : *::*:** : . . . .	: *::*:** : . . . .	: ** : *::*:** : . . . .
		ITAM	DOCK motif
hCLASP4	FEAPYTLSGKKQGCIEEQCKRRTILT	TSNSFYVVKH	RIPINCEQQINLKPIDGATDEIKD 1859
hCLASP5	YTFPTLEGRPRGELHEQYRRNTVLT	TMHAFYIK	TRISVIQKEEFVLTPIEVAIEDMKK 1870
hCLASP3	YCTPFTLDGRAHGEHEQFKRKTILT	TSHAFYIK	TRVNVTHKEEILTPIEVAIEDMQK 1992
hCLASP2	FEMPFTQTGKRQGGVEEQCKRRTILT	AIHCFYVVKH	RIPVMYQHHTDLNPIEVAIDEMSK 1830
hCLASP7	FCTPFTPDGRAHGEHEQHKRKTLLS	TDHAFYIK	TRIRVCHREETVLTPEVAIEDMQK 1911
hCLASP1	FETPFTLSGKKHGGVAEQCKRRTILT	TSHLFYVVKH	RIRIQVISQSSTELNPIEVAIDEMSR 2032
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		Coiled-coil	
hCLASP4	KTAELQKLCSSSTDVDMIQLQLKLC	QWVSQVQV	NAGPLAYARAFLNDSQASKYPPKKVSELK 1919
hCLASP5	KTQLQAVAINQEPDDAKMLQMVLC	QSVGATVN	QGPLEVAQVFLAEIPADPKLYRHHNKL 1930
hCLASP3	KTQLAFATHQDPPADPKMLQMVLC	QSVGTTVN	QGPLEVAQVFLSEIPSDPKLFRHHNKL 2052
hCLASP2	KVAELRQLCSSAEVDMIKLQLKLC	QSVSQVQV	NAGPLAYARAFLLDNTNKRYPDNKVKLLK 1890
hCLASP7	KTRELAFAEQDPPDAKMLQMVLC	QSVGPTVN	QGPLEVAQVFLAEIPEDPKLFRHHNKL 1971
hCLASP1	KVSELNQLCTMEEVDMISLQLKLC	QSVSVKVN	NAGPMAYARAFLEETNAKKYPDNQVKLLK 2092
	: . : * : * : * : * : * : *	: . : * : * : * : * : * : *	: . : * : * : * : * : * : *
		Coiled-coil	
hCLASP4	DMFRKFIOACSALELNERLIKEDQVEY	HEGLKSNFRDMVKELSD	IIHEQILOEDTMHSP 1979
hCLASP5	LCFKEFIMRCGLAVEKNKRLITADQREY	QOELKKYNKLNKLENLRPM	IERKIPELYKPIFR 1990
hCLASP3	LCFKDFTKRCEDALRNKSLIGPVQKEY	QRELGLKSSP	----- 2090
hCLASP2	EVFRQFVEACGOALAVNERLIKEDQLEY	QOEMKANYREMAKELSE	IMHEQICPLEEKTS- 1949
hCLASP7	LCFKDFCKCEDALRNKALIGPDQKEYH	RELERNYCRLREALQPI	LTLQRLPQLMAPTP- 2030
hCLASP1	EIFRQFADACGOALDVNERLIKEDQLEY	QOELRSHYKMDLSELSTV	MEQITGRDDLSKR 2152
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		PDZ ligand	
hCLASP4	WMSNTLHVFCASISGTSSDRGYGSP	RYAEV	-- 2008
hCLASP5	VESQKRDSFHRSSFRCETQLSQGS	-----	2015
hCLASP3	-----	-----	-----
hCLASP2	VLPNSLHIFNAISGTPSTMVHGMTSS	SSVV	1980
hCLASP7	--PGLRNSLNRASFRKADL	-----	2047
hCLASP1	GVDOTCTRVISKATPALPTVISISS	SAEV	-- 2180